

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 15:52:02 ; Search time 312 Seconds
(without alignments)
8046.402 Million cell updates/sec

Title: US-09-884-814-2
Perfect score: 930
Sequence: 1 atcgctgggtcgaagccac.....ccgagagctccctctga 930

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N Genesec 19jun03:*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
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- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	930	100.0	930	20	AAZ19968
2	930	100.0	930	21	AAZ50624
3	930	100.0	1024	25	ABZ83750
4	930	100.0	1105	20	AAZ99434
5	930	100.0	1105	21	AAZ29323
6	930	100.0	1105	22	AAZ14819
7	930	100.0	1105	22	AAZ02388
8	930	100.0	1643	24	AAZ94928

9	928.4	99.8	930	20	AAZ99435	UCP2 Nucleotide se
10	928.4	99.8	930	24	ABK86151	CDNA encoding huma
11	928.4	99.8	1596	20	AAV82381	Full length human
12	928.4	99.8	1596	21	AAA99716	Mouse body weight-
13	928.4	99.8	1596	21	AAA52254	Human uncoupling p
14	928.4	99.8	1612	19	AAV4595	Human respiration
15	928.4	99.8	1682	21	AAZ29244	Human mitochondria
16	928.4	99.8	1888	20	AAZ99436	UCP2 nucleotide se
17	928.4	99.8	1888	20	ABK84483	Human CDNA differe
18	928.4	99.8	1255	19	AAV09078	Human C5 gene CDNA
19	893.6	96.1	1255	17	AAZ13981	Human body weight
20	880.4	94.7	960	22	AAZ3793	Hybrid hUCP2 DNA.
21	762	81.9	1575	24	ABK3772	Rat sequence diffe
22	618	66.5	1205	19	AAV09077	Mouse C5 gene full
23	618	66.5	1205	19	AAV82380	Full length mouse
24	618	66.5	1205	21	AAA99715	Mouse body weight-
25	618	66.5	1205	21	AAA52253	Mouse uncoupling p
26	614.8	54.7	1205	17	AAZ13980	Brown fat uncoupli
27	508.8	54.7	512	24	ABK38976	CDNA encoding lung
28	508.8	54.7	512	25	ACA11305	Human lung adenoca
29	508.8	54.7	512	25	ACA02491	Lung cancer therap
30	474	51.0	939	22	AAZ19969	Human uncoupling p
31	474	51.0	939	22	AAH18849	Human UCP3 CDNA.
32	474	51.0	1175	21	AAZ29245	Human mitochondria
33	474	51.0	1231	19	AAV72690	Human uncoupling p
34	474	51.0	1231	24	ABO72999	Mouse uncoupling p
35	473.4	50.9	1204	19	AAV71712	Mouse uncoupling p
36	473.4	50.9	1658	19	AAV84307	Mouse uncoupling p
37	472.4	50.8	1193	20	AAV54602	Human uncoupling p
38	472.4	50.8	1193	21	AAZ46055	Human uncoupling a hu
39	472.4	50.8	1193	22	AAZ08530	Human uncoupling p
40	472.4	50.8	1193	22	AAZ08530	Human mitochondria
41	472.4	50.8	1220	19	AAV71710	Human uncoupling p
42	471.8	50.7	2782	20	AAZ07060	Mouse uncoupling p
43	471.8	50.7	2782	20	AAV71227	CDNA encoding a mu
44	471.8	50.7	2782	21	AAZ90318	CDNA encoding multi
45	471.8	50.7	2782	22	AAZ09318	Mouse uncoupling p

ALIGNMENTS

RESULT 1
AAZ19968 standard; CDNA; 930 BP.

ID	AAZ19968	standard; CDNA; 930 BP.
XX	AAZ19968:	
AC	AAZ19968:	
XX	21-DEC-1999 (first entry)	
DT	21-DEC-1999 (first entry)	
XX	Human uncoupling protein 2 CDNA.	
DE	Human uncoupling protein 2 CDNA.	
XX	Uncoupling protein 2; UCP2; human; obesity; diabetes; diagnosis;	
KW	gene therapy; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	Variation	replace(164,T)
FT		/tag= a
XX		
PN	NO9948905-A1.	
XX		
XX	30-SEP-1999.	
XX		
PF	23-MAR-1999;	99WO-US06317.
XX		
PR	23-MAR-1998;	98US-0078972.
XX		
PA	(MUSC-) MUSC POUND RES DEV.	
XX		
PI	Garvey WT, Argyropoulos G;	
XX		

XX Sequence 930 BP; 185 A; 286 C; 255 G; 204 T; 0 other;

Query Match 100.0%; Score 930; DB 21; Length 930;
Best Local Similarity 100.0%; Pred. No. 3, 6e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTTGGGTTCAAGGCCACAGATGTCCTCCCTACTGACCTGTAAGTTCTTGAGGCT 60
   |||||
DB 1 ATGTTGGGTTCAAGGCCACAGATGTCCTCCCTACTGACCTGTAAGTTCTTGAGGCT 60
   |||||
QY 61 GGCACAGCTGCTCGATCGCAGATCTCATACCTTTCTCTGTAATGCTAAATCCG 120
   |||||
DB 61 GGCACAGCTGCTCGATCGCAGATCTCATACCTTTCTCTGTAATGCTAAATCCG 120
   |||||
QY 121 TTACAGATCCAAAGGAAAGTGAAGGCGCAGTGCAGCTACAGCAGGCGCCAGTACCG 180
   |||||
DB 121 TTACAGATCCAAAGGAAAGTGAAGGCGCAGTGCAGCTACAGCAGGCGCCAGTACCG 180
   |||||
QY 181 GGTGTATGGGACCACTTGTGACCATGTGCGTACTGAGGSCCCCGAAGCTTACAT 240
   |||||
DB 181 GGTGTATGGGACCACTTGTGACCATGTGCGTACTGAGGSCCCCGAAGCTTACAT 240
   |||||
QY 241 GGGCTGTGCTGGCGCTGAGCGCCAAATGAGCTTGTCTGTCCGATGCGCTGTAT 300
   |||||
DB 241 GGGCTGTGCTGGCGCTGAGCGCCAAATGAGCTTGTCTGTCCGATGCGCTGTAT 300
   |||||
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   |||||
DB 301 GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGCATGCGAGATTGGAGCGGCTC 360
   |||||
QY 361 CTAGCAGGACGACCAACAGTGCCTTGTGCTGTGCTGTGCGCCACGCCAGTGTGTA 420
   |||||
DB 361 CTAGCAGGACGACCAACAGTGCCTTGTGCTGTGCTGTGCGCCACGCCAGTGTGTA 420
   |||||
QY 421 AAGGTCGATTCGAAGCTCAGGCGCGGCTGAGGTGTGCGAGTATACCAAGCACGTC 480
   |||||
DB 421 AAGGTCGATTCGAAGCTCAGGCGCGGCTGAGGTGTGCGAGTATACCAAGCACGTC 480
   |||||
QY 481 AATGCTTACAAGACCTTGTGCGAGAGAGAGGCTTCCGAGCTTCTGAAAAGGACCTCT 540
   |||||
DB 481 AATGCTTACAAGACCTTGTGCGAGAGAGAGGCTTCCGAGCTTCTGAAAAGGACCTCT 540
   |||||
QY 541 CCCAATGTTGCTGTATGCACTTGTGCACTGTGCTGAGTGTGTAAGTATGACCTATC 600
   |||||
DB 541 CCCAATGTTGCTGTATGCACTTGTGCACTGTGCTGAGTGTGTAAGTATGACCTATC 600
   |||||
QY 601 AAGGATGCCCTCTCTGAAGCCCACTCATGACATGACATGACCTTCCACTTCACTTCT 660
   |||||
DB 601 AAGGATGCCCTCTCTGAAGCCCACTCATGACATGACATGACCTTCCACTTCACTTCT 660
   |||||
QY 661 GCGTTTGGGAGGAGCTTGTGCACTGTGCACTGTGCTGAGTGTGTAAGTATGACCT 720
   |||||
DB 661 GCGTTTGGGAGGAGCTTGTGCACTGTGCACTGTGCTGAGTGTGTAAGTATGACCT 720
   |||||
QY 721 AGATACATGAACCTTGTGCGAGGACATGACAGTACAGTACGCTGACCTTACCATG 780
   |||||
DB 721 AGATACATGAACCTTGTGCGAGGACATGACAGTACAGTACGCTGACCTTACCATG 780
   |||||
QY 781 CTTCAGAGAGAGAGGAGGCGCGGAGCTTCTTCAAGAGGTTCAAGGCTTCTTCCGCTG 840
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DB 781 CTTCAGAGAGAGAGGAGGCGCGGAGCTTCTTCAAGAGGTTCAAGGCTTCTTCCGCTG 840
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QY 841 GGTTCCTGGAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
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DB 841 GGTTCCTGGAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
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QY 901 GCGTGAATTCCTCGAGAGAGGCTCCTTTCTTA 930
   |||||
DB 901 GCGTGAATTCCTCGAGAGAGGCTCCTTTCTTA 930
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RESULT 3

ABZ83760
ID ABZ83760 standard, cDNA, 1024 BP.

XX AC ABZ83760;

XX 14-MAY-2003 (first entry)

XX Toxicologically relevant human nucleotide sequence #919.

XX Toxicologically relevant gene; toxicological response; gene; ss.

XX Homo sapiens.

XX WO2003016500-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002MO-US26514.

XX 16-AUG-2001; 2001US-313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweisler K;

XX Alen P;

XX WPI, 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening

XX of drugs, comprises comparing the expression profile of one or more

XX human toxic response genes to a reference gene expression profile

XX indicative of toxicity -

XX Claim 1; Page 284; 455BP; English.

XX The present invention describes a method (M1) for determining a

XX toxicological response to an agent, which comprises comparing the

XX expression profile of one or more human toxic response genes to a

XX reference gene expression profile indicative of toxicity, and so

XX determining the presence of a toxic response to the agent. Also

XX described: (1) an array comprising one or more polynucleotides selected

XX from the genes corresponding to the partial sequences given in ABZ82842

XX to ABZ84764, or their fragments of at least 20 nucleotides, or

XX homologues; and (2) determining if a gene putatively identified to be a

XX toxic response gene plays a role on toxic response pathways by

XX determining the expression profile of the gene after exposure of cells

XX or a human subject to a known toxic pharmaceutical or industrial agent,

XX comprising: (a) exposing cells to an agent or isolating cells from a

XX human subject who was exposed to an agent; (b) obtaining the test gene

XX expression profile for a putatively identified toxic response gene after

XX exposure to a known toxic pharmaceutical or industrial agent; and

XX (c) comparing the test profile to the expression profile of a gene with

XX a similar function or comparing the test profile to the expression

XX profile of that gene after exposure to other known toxic compounds. The

XX methods are useful for predicting and determining toxicological responses

XX on a cellular, organ or system level. The arrays comprising the human

XX CC genes are useful for toxicological screening of drugs, pharmaceutical

XX compounds and chemicals.

XX Sequence 1024 BP; 200 A; 314 C; 274 G; 236 T; 0 other;

Query Match 100.0%; Score 930; DB 25; Length 1024;
Best Local Similarity 100.0%; Pred. No. 3, 7e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTTGGGTTCAAGGCCACAGATGTCCTCCCTACTGACCTGTAAGTTCTTGAGGCT 60
   |||||
DB 89 ATGTTGGGTTCAAGGCCACAGATGTCCTCCCTACTGACCTGTAAGTTCTTGAGGCT 148
   |||||
QY 61 GGCACAGCTGCTCGATCGCAGATCTCATACCTTTCTCTGTAATGCTAAAGTCCG 120
   |||||
DB 149 GGCACAGCTGCTCGATCGCAGATCTCATACCTTTCTCTGTAATGCTAAAGTCCG 208
   |||||

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QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCGCAGTACCGC 180
DB 209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCGCAGTACCGC 268
QY 181 GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCCGGAAGCTCTACAT 240
DB 269 GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCCGGAAGCTCTACAT 328
QY 241 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGACATCGGCTGTAT 300
DB 329 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGACATCGGCTGTAT 388
QY 301 GATTCGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCCAGCATTTGGAGCGCTTC 360
DB 389 GATTCGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCCAGCATTTGGAGCGCTTC 448
QY 361 CTAGCAGGACAGACAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 420
DB 449 CTAGCAGGACAGACAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 508
QY 421 AAGGTCGATTCCAAGCTCAAGCCCGGCTGGAGTGGTGGAGATACCAAGCACCTGTC 480
DB 509 AAGGTCGATTCCAAGCTCAAGCCCGGCTGGAGTGGTGGAGATACCAAGCACCTGTC 568
QY 481 AATGGCTCAAGACCATTTGCCGAGAGGAGGTTCCGGGGCTCTGGAAAGGACCTCT 540
DB 569 AATGGCTCAAGACCATTTGCCGAGAGGAGGTTCCGGGGCTCTGGAAAGGACCTCT 628
QY 541 CCCAATGTTGCTGTATGCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 600
DB 629 CCCAATGTTGCTGTATGCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 688
QY 601 AAGGATGCTCTCTCTTAAGCCCACTCAATGACATGACCTCTCTCTCTCTCTCTCTCT 660
DB 689 AAGGATGCTCTCTCTTAAGCCCACTCAATGACATGACCTCTCTCTCTCTCTCTCTCT 748
QY 661 GCCTTTGGGGCAGGCTTCTGACACACTGTACCTGCTCTCTCTCTCTCTCTCTCTCT 720
DB 749 GCCTTTGGGGCAGGCTTCTGACACACTGTACCTGCTCTCTCTCTCTCTCTCTCTCT 808
QY 721 AGATACATGAATCTCTGCTGGGCGGACGATGAGCTGGCCCTGTCGCTTACCATG 780
DB 809 AGATACATGAATCTCTGCTGGGCGGACGATGAGCTGGCCCTGTCGCTTACCATG 868
QY 781 CTCGAGAGAGAGGAGGAGGCTTCTACCAAGGATCATGCCCTCTCTCTCTCTCTCT 840
DB 869 CTCGAGAGAGAGGAGGAGGCTTCTACCAAGGATCATGCCCTCTCTCTCTCTCTCT 928
QY 841 GGTTCCTGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 929 GGTTCCTGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 988
QY 901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930
DB 989 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 1018

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RESULT 4
ID AAX9434 standard; DNA; 1105 BP.
XX AAX9434.

AC AAX9434.
XX 19-OCT-1999 (first entry)
XX UCP2 Nucleotide sequence.
XX un coupling protein; nucleotide; mitochondria; diabetes;
XX brown adipose tissue; wild type; obesity; thermo-regulation; de.
OS Homo sapiens.
XX
XX MO9937812-A1.

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XX 29-JUL-1999.
PD 21-JAN-1999; 99MO-US01198.
XX 21-JAN-1999; 99MO-US01198.
XX 23-JAN-1998; 98US-0012218.
XX (ORCH-) ORCHID BIOCOMPUTER INC.
PA Violijk LP;
PI WPI: 1999-469144/39.
XX P-PSDB; AAY28351.
DR A novel single nucleotide polymorphism of the uncoupling protein 2
XX gene, useful for diagnosis, prognosis and treatment of obesity
XX
XX Disclosure; Fig 2; 68pp; English.
XX
XX This is the nucleotide sequence of uncoupling protein-2 (UCP-2) as
XX reported by Boss et al, FEBS Lett 408, 39-42, 1997. (thymine at
XX identifying a UCP2 polymorphism, especially Val55 (thymine at
XX nucleotide 164), can be used to diagnose obesity, non-insulin dependent
XX diabetes mellitus and other UCP2 related diseases. Wild-type UCP2
XX generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2
XX related diseases include atherosclerosis, hyperinsulinemia, chronic
XX inflammation, thermogenesis, apoptosis and cachexia.
XX
XX Sequence 1105 BP; 205 A; 345 C; 287 G; 268 T; 0 other;
SQ

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Query Match 100.0%; Score 930; DB 20; Length 1105;
Best Local Similarity 100.0%; Pred. No. 3; 8e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTTGGGTTCAAGGACCAAGATGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
DB 89 ATGTTGGGTTCAAGGACCAAGATGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148
QY 61 GGCACACCTGCTGATCGAGATCTCATACCTTCTCTGATACCTGCTTAAGTCCGG 120
DB 149 GGCACACCTGCTGATCGAGATCTCATACCTTCTCTGATACCTGCTTAAGTCCGG 208
QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTGACAGCCAGCCCGCAGTACCGC 180
DB 209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTGACAGCCAGCCCGCAGTACCGC 268
QY 181 GGTGTGATGGGACCACTTCTGACCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 269 GGTGTGATGGGACCACTTCTGACCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 328
QY 241 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGATCGGCTGTAT 300
DB 329 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGATCGGCTGTAT 388
QY 301 GATTCGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCCAGCATTTGGAGCGCTTC 360
DB 389 GATTCGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCCAGCATTTGGAGCGCTTC 448
QY 361 CTAGCAGGACAGACAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 420
DB 449 CTAGCAGGACAGACAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 508
QY 421 AAGGTCGATTCCAAGCTCAAGCCCGGCTGGAGTGGTGGAGATACCAAGCACCTGTC 480
DB 509 AAGGTCGATTCCAAGCTCAAGCCCGGCTGGAGTGGTGGAGATACCAAGCACCTGTC 568
QY 481 AATGGCTCAAGACCATTTGCCGAGAGGAGGTTCCGGGGCTCTGGAAAGGACCTCT 540
DB 569 AATGGCTCAAGACCATTTGCCGAGAGGAGGTTCCGGGGCTCTGGAAAGGACCTCT 628
QY 541 CCCAATGTTGCTGTATGCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 600
DB 629 CCCAATGTTGCTGTATGCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 688

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QY 601 AAGATGCCCTCCTGAAAGCCAACTCATGAGATGACTCCCTTGGCACTTCT 660
 DB 689 AAGATGCCCTCCTGAAAGCCAACTCATGAGATGACTCCCTTGGCACTTCT 748
 QY 661 GCCTTGGGAGAGGCTTCTGCAACAATGATGAGCTCCCTTGAAGAGAG 720
 DB 749 GCCTTGGGAGAGGCTTCTGCAACAATGATGAGCTCCCTTGAAGAGAG 808
 QY 721 AGATACATGAATCTTCCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 809 AGATACATGAATCTTCCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 866
 QY 781 CTCGAG 840
 DB 869 CTCGAG 928
 QY 841 GGTTCCTGAAAGCTGTGTGATGTTCTGACCTTATGAGAGAGAGAGAGAG 900
 DB 929 GGTTCCTGAAAGCTGTGTGATGTTCTGACCTTATGAGAGAGAGAGAGAG 988
 QY 901 GCCTGACCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
 DB 989 GCCTGACCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018

RESULT 5

AAZ29323 standard; cDNA; 1105 BP.

AAZ29323;

29-FEB-2000 (first entry)

Human uncoupling protein-2 cDNA.

Human uncoupling protein-2; UCP; immune response; electron transport;

oxidative phosphorylation; Major histocompatibility complex;

MHC class II HLA-DR; Proton motor force; mitochondrial membrane potential;

mitochondrial metabolism; cancer; autoimmune disease;

neurodegenerative disorder; ds.

Homo sapiens.

Key

CDS

Location/Qualifiers

89..1018

/*tag= a

/product= "Human uncoupling protein-2"

W0953953-A2.

28-OCT-1999.

30-MAR-1999; 99WO-US06874.

17-APR-1998; 98US-0082250.

29-JUL-1998; 98US-0094519.

24-SEP-1998; 98US-0101580.

(UYVE-) UNIV VERMONT.

Newell MK;

WPI; 2000-096773/08.

P-PDB; AAY44292.

CC the reversible uncoupling of electron transport and oxidative
 CC phosphorylation, which leads to a decrease in the mitochondrial membrane
 CC potential. This can induce lysis in a tumor cell by inducing the
 CC expression of MHC class II HLA-DR. These methods can be used for
 CC regulating cell growth and division to control disease processes by
 CC manipulating mitochondrial metabolism and the expression of cell surface
 CC immune proteins. They can be used for treating diseases associated with
 CC excessive cellular division, aberrant differentiation, and premature
 CC cellular death, e.g. cancers, autoimmune diseases, neurodegenerative
 CC disorders etc.
 XX
 SQ Sequence 1105 BP; 205 A; 345 C; 287 G; 268 T; 0 other;

Query Match 100.0%; Score 930; DB 21; Length 1105;
 Best Local Similarity 100.0%; Pred. No. 3,8e-239;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTGGGCTTCAAGGCGCAGATGTCCTCCCTGAGAGAGAGAGAGAGAG 60
 DB 89 AAGTTGGGCTTCAAGGCGCAGATGTCCTCCCTGAGAGAGAGAGAGAGAG 148
 QY 61 GGCACAGCTGCTGATGAGAGATCTATCACTTCTCTGATGATGATGATGAT 120
 DB 149 GGCACAGCTGCTGATGAGAGATCTATCACTTCTCTGATGATGATGATGAT 208
 QY 121 TTACAGATCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 DB 209 TTACAGATCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 268
 QY 181 GGTGTGATGAGGACCATTTCTGACATGATGATGATGATGATGATGATGAT 240
 DB 269 GGTGTGATGAGGACCATTTCTGACATGATGATGATGATGATGATGATGAT 328
 QY 241 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 329 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 388
 QY 301 GATTCGTCAACAGCTTCTACACCAAGGCTCTGAGCATGAGCATGAGCATGAG 360
 DB 389 GATTCGTCAACAGCTTCTACACCAAGGCTCTGAGCATGAGCATGAGCATGAG 448
 QY 361 CTAG 420
 DB 449 CTAG 508
 QY 421 AAGTCCGATTCAG 480
 DB 509 AAGTCCGATTCAG 568
 QY 481 AATGCTTACAG 540
 DB 569 AATGCTTACAG 628
 QY 541 CCCAATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 629 CCCAATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
 QY 601 AAGAGTCCCTCTGAAAGCCAACTCATGAGATGAGATGAGATGAGATGAGAT 660
 DB 689 AAGAGTCCCTCTGAAAGCCAACTCATGAGATGAGATGAGATGAGATGAGAT 748
 QY 661 GCCTTGGGAG 720
 DB 749 GCCTTGGGAG 808
 QY 721 AGATACATGAATCTTCCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 809 AGATACATGAATCTTCCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
 QY 781 CTCGAG 840
 DB 869 CTCGAG 928

The present sequence encodes human uncoupling protein-2. UCPS can cause

XX	Human; uncoupling protein; UCP-2; cancer; brain; renal; antiviral;
KW	antibacterial; antifungal; cytostatic; immunosuppressive; scleroderma;
KW	antiarrhythmic; dermatological; UCP inhibitor; therapy; antirheumatic;
KW	rheumatoid arthritis; leukemia; tumour; autoimmune disease; SLE;
KW	systemic lupus erythematosus; celliac disease; infectious disease;
KW	pemphigus vulgaris; ss.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Location/Qualifiers
FT	89..1018
FT	CDS
FT	/*tag= a
FT	/product= "Human UCP-2 protein"
XX	
PN	MO200078941-A2.
XX	
PD	28-DEC-2000.
XX	
PF	22-JUN-2000; 2000MO-US17245.
XX	
PR	23-JUN-1999; 99US-0140574.
XX	
PA	(UYVE-) UNIV VERMONT & STATE AGRIC COLLAGE.
XX	
P1	Newell MK;
XX	
DR	WPI; 2001-102716/11.
DR	P-PSDB; AAY72342.
XX	
PT	Inhibiting plasma membrane uncoupling protein expression in tumor cells
PT	and rapidly dividing bacterial cells, for treating cancer and
PT	infectious diseases -
XX	
PS	Disclosure; Page 104; 106pp; English.
XX	
CC	The present sequence is a cDNA encoding human Uncoupling Protein.
CC	UCP-2. The present invention relates to a method for inhibiting the
CC	expression of plasma membrane uncoupling protein (UCP) in a cell by a
CC	plasma membrane UCP inhibitor. UCP is expressed on lysosomal membranes
CC	and plasma membranes of rapidly dividing cells, but absent in growth
CC	arrested or chemotherapy resistant cells. This method is useful in the
CC	inhibition of plasma membrane UCP expression in tumor cells,
CC	lymphocytes, pancreatic beta cells, rapidly dividing bacterial cells
CC	or B cells. UCP inhibitor is useful in the prevention and treatment of
CC	infectious disease, rheumatoid arthritis, scleroderma and cancers such
CC	as brain cancer, leukemia, renal cancer, and tumors. The UCP activator
CC	is useful in the treatment of autoimmune diseases such as systemic
CC	lupus erythematosus (SLE), celliac disease and pemphigus vulgaris. UCP
CC	is also useful for inducing cellular division in nerve cells.
XX	
8Q	Sequence 1105 BP; 205 A; 345 C; 287 G; 268 T; 0 other;
XX	
Query Match	100.0%; Score 930; DB 22; Length 1105;
Best Local Similarity	100.0%; Pred. No. 3.8e-219;
Matches 930; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	1 ATGGTTGGGTTTCAAGGCCACAGATGTGCCCCCTACATGCACTGAGAGTTTCTTGAGGAGCT 60
DB	89 ATGGTTGGGTTTCAAGGCCACAGATGTGCCCCCTACATGCACTGAGAGTTTCTTGAGGAGCT 148
QY	61 GGCAACAGCTCCTGCATCGCAGATCTCATCACTTTCTCTGTGATAGTGTAAAGTCGG 120
DB	149 GGCAACAGCTCCTGCATCGCAGATCTCATCACTTTCTCTGTGATAGTGTAAAGTCGG 208
QY	121 TTACAGATCCAAAGAGAAAGTCAAGGGGCCAGTGGCCGCTAAGCCAGCCAGTACCGC 180
DB	209 TTACAGATCCAAAGAGAAAGTCAAGGGGCCAGTGGCCGCTAAGCCAGCCAGTACCGC 268
QY	181 GGTGTGATGGGCAACATTTGACCAATGTGTGCTGATAGAGGCCCCCGACACCTCTACAA 240
DB	269 GGTGTGATGGGCAACATTTGACCAATGTGTGCTGATAGAGGCCCCCGACACCTCTACAA 328
QY	241 GGAGCTGGTTCGCGCCTGCAGCGCCCAATGAGCTTGGCTCTGTCCGATCGGCTGTAT 300

Db	329	GGGCTGGTGGCCGGCTCGACGGCCAAATGAGTTTGGCTCTGTCTCGAGTCGGCTGTT
Qy	301	GATTTCGTCAAACAGTTTCTACACAAAGGGCTCTGAGATGACCAAGCATTTGGAGCCGGCC
Db	389	GATTTCGTCAAACAGTTTCTACACAAAGGGCTCTGAGATGACCAAGCATTTGGAGCCGGCC
Qy	361	CTAGACAGCAGACACACAGAGTCCTGGCTGTGGCTGTGGCCAGCCACGATGTGG
Db	449	CTAGACAGCAGACACACAGAGTCCTGGCTGTGGCTGTGGCCAGCCACGATGTGG
Qy	421	AAGTTCGCATTCGAAGCTGAGCCCGGGCTGAGAGTGTGTGAGATACCAAGACACGG
Db	509	AAGTTCGCATTCGAAGCTGAGCCCGGGCTGAGAGTGTGTGAGATACCAAGACACGG
Qy	481	AATGCTCTACAAAGCACTTGCCTCCGAGAGGAAAGGTTCCGGGGCTCTGGAAAAGGACCT
Db	569	AATGCTCTACAAAGCACTTGCCTCCGAGAGGAAAGGTTCCGGGGCTCTGGAAAAGGACCT
Qy	541	CCCAATGTTGCTGTATGSCAATTTGTCAACTGTGTGAGCTGGTGACTTATGACCTCA
Db	629	CCCAATGTTGCTGTATGSCAATTTGTCAACTGTGTGAGCTGGTGACTTATGACCTCA
Qy	601	AAGATGCGCTCTCCGAAAGCAACCTCACTGACAGATGACATGACCTCCCTGGACACTTACCT
Db	689	AAGATGCGCTCTCCGAAAGCAACCTCACTGACAGATGACATGACCTCCCTGGACACTTACCT
Qy	661	GCTTTGGGGGAGGCTTTGTGACACACTGTCACTGCCCTCCCTGTAGACGTGTGACAG
Db	749	GCTTTGGGGGAGGCTTTGTGACACACTGTCACTGCCCTCCCTGTAGACGTGTGACAG
Qy	721	AATATCATTGAACCTGTGCTCTGGGCCCAATGACGTATGCGCTTGGCACTGTGCCCTTACCCA
Db	809	AATATCATTGAACCTGTGCTCTGGGCCCAATGACGTATGCGCTTGGCACTGTGCCCTTACCCA
Qy	781	CTCCAGAGAGAGGGGGCCCCGAGACCTTTACAAAGGTTCAAGCCCTCTTCTCGGCT
Db	869	CTCCAGAGAGAGGGGGCCCCGAGACCTTTACAAAGGTTCAAGCCCTCTTCTCGGCT
Qy	841	GGTTCCTGGAAAGCTGTGTGATTTGTTCATCACTATGACGATGAACGAGCCTTCATGG
Db	929	GGTTCCTGGAAAGCTGTGTGATTTGTTCATCACTATGACGATGAACGAGCCTTCATGG
Qy	901	GCTGTCACTTCCGAGAGGCTCCCTTCTGA 930
Db	989	GCTGTCACTTCCGAGAGGCTCCCTTCTGA 1018
RESULT 8		
AAS94928		
ID	AAS94928	strand; DNA, 1643 BP.
AC	AAS94928;	
XX	14-FEB-2002	(first entry)
DE	Human DNA sequence #183 expressed during foam cell differentiation.	
KM	Human; foam cell differentiation; atherosclerosis; cerebral stroke;	
KM	cardiovascular disorder; coronary artery disease; gene therapy; ds	
XX	Homo sapiens.	
XX	WO200177389-A2.	
PD	18-OCT-2001.	
XX	04-APR-2001; 2001WO-US11128.	
XX	05-APR-2000; 2000US-195106P.	
PA	(INCY-) INCYTE GENOMICS INC.	


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QY 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
DB 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
QY 61 GGCACAGCTGCTGTCATCGCATATCTACACCTTCTCTTGGAATCTGTAAGTCCGG 120
DB 61 GGCACAGCTGCTGTCATCGCATATCTACACCTTCTCTTGGAATCTGTAAGTCCGG 120
QY 121 TTACAGATCCCAAGAGAAAGTCAAGGGCCAGTCCGGCTACAGCAGGCGCCAGTACCGC 180
DB 121 TTACAGATCCCAAGAGAAAGTCAAGGGCCAGTCCGGCTACAGCAGGCGCCAGTACCGC 180
QY 181 GGTGTGATGGGACCACTTCTGACCATGTGTGCTGTAAGGCGCCGAAAGCTTCTACAT 240
DB 181 GGTGTGATGGGACCACTTCTGACCATGTGTGCTGTAAGGCGCCGAAAGCTTCTACAT 240
QY 241 GGGCTGGTTGCCGGCTGAGAGCGCCAAATGAGCTTGTGCTGTCCGGATGGGCTGTAT 300
DB 241 GGGCTGGTTGCCGGCTGAGAGCGCCAAATGAGCTTGTGCTGTCCGGATGGGCTGTAT 300
QY 301 GATTCTGTCAAAACAGTTCTACACAAAGGCTCTGAGCATGCCAGATTGGAGCGGCTC 360
DB 301 GATTCTGTCAAAACAGTTCTACACAAAGGCTCTGAGCATGCCAGATTGGAGCGGCTC 360
QY 361 CTAGCAGGCGACCAAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 CTAGCAGGCGACCAAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 AAGGTCGATTCGAAGCTCAGAGCGCGGCTGAGAGTGTCTGAGATACCAAGACCGTCT 480
DB 421 AAGGTCGATTCGAAGCTCAGAGCGCGGCTGAGAGTGTCTGAGATACCAAGACCGTCT 480
QY 481 AATGCTTCAAGACCAATGCTGCGAGAGAGAGGTTCCGGGCTCTGGAAGAGGACCTCT 540
DB 481 AATGCTTCAAGACCAATGCTGCGAGAGAGAGGTTCCGGGCTCTGGAAGAGGACCTCT 540
QY 541 CCCAATGTTGCTGTATGATGCACTGTCAGTGTGCTGAGCTGTGATGATGACCTCATC 600
DB 541 CCCAATGTTGCTGTATGATGCACTGTCAGTGTGCTGAGCTGTGATGATGACCTCATC 600
QY 601 AAGGATGCTCTCTGAAAGCAACTCATGATGACATGACCTCTCTGCACTTCACTTCT 660
DB 601 AAGGATGCTCTCTGAAAGCAACTCATGATGACATGACCTCTCTGCACTTCACTTCT 660
QY 661 GCGTTTGGGCGAGGCTTGTGACCACTGTCATGCGCTCCCTGTGAGCGTGTCAAGCG 720
DB 661 GCGTTTGGGCGAGGCTTGTGACCACTGTCATGCGCTCCCTGTGAGCGTGTCAAGCG 720
QY 721 AGATACATGAATCTGCTGCTGAGGCAAGTACAGTACGCTGAGCACTGCTTACATG 780
DB 721 AGATACATGAATCTGCTGCTGAGGCAAGTACAGTACGCTGAGCACTGCTTACATG 780
QY 781 CTCCAGAGAGAGGCGCGGAGCTTCTCAAAAGGTTATGCGCTTCTGCGCTG 840
DB 781 CTCCAGAGAGAGGCGCGGAGCTTCTCAAAAGGTTATGCGCTTCTGCGCTG 840
QY 841 GGTCTCTGAAGCTGTGATGTCTGACCTATGAGCAGCTGAAAGCGCTCATGCT 900
DB 841 GGTCTCTGAAGCTGTGATGTCTGACCTATGAGCAGCTGAAAGCGCTCATGCT 900
QY 901 GCTTGCATCTCCGAGAGGCTCTCTTCTGA 930
DB 901 GCTTGCATCTCCGAGAGGCTCTCTTCTGA 930

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RESULT 10

ABK86151

ID ABK86151 standard; cDNA; 930 BP.

XX AC ABK86151;

XX 26-AUG-2002 (first entry)

XX

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DE cDNA encoding human uncoupling protein UCP-2.
XX
KW Human; uncoupling protein; UCP-2; stroke; ischaemia; epilepsy;
KW neurological disorder; neuronal injury; Parkinson's disease;
KW Huntington's disease; inherited ataxia; motor neuron disease;
KW Alzheimer's disease; traumatic brain injury; bradykinin;
KW serotonin; histamine; arachidonic acid; gene; chromosome 11; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..930
FT /tag=a
FT /product="Uncoupling protein UCP-2"
XX
PD WO200236829-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US45744.
XX
PR 01-NOV-2000; 2000US-244946P.
XX
PA (AGT-) AGY THERAPEUTICS INC.
XX
PI Gonzalez-Zulueta M, Shamloo M, McFarland KC, Chin D, Wieloch T;
PI Melcher T;
XX
DR MPI; 2002-490012/52.
DR P-PSDB; AAU98901.
XX
PT Diagnosing occurrence of stroke or assessing a patient's susceptibility
PT to stroke, by detecting in a patient sample an elevated level of
PT uncoupling proteins-2 expression -
XX
PS Disclosure; Page 79; 80pp; English.
XX
CC The invention relates to a method of diagnosing occurrence of a stroke or
CC assessing a patient's susceptibility to a stroke, comprising detecting in
CC a patient sample an elevated level of uncoupling proteins (UCP)-2
CC expression. The method is useful for diagnosing occurrence of a stroke or
CC assessing a patient's susceptibility to a stroke, where the stroke is an
CC ischemic stroke. The method is useful for treating a subject having or
CC is susceptible to a neurological disorder or a neuronal injury, where the
CC neuronal injury is a stroke, or an ischemic stroke. The neurological
CC disorder is selected from Parkinson's disease, Huntington's disease,
CC inherited ataxia, motor neuron diseases, Alzheimer's disease, epilepsy,
CC and traumatic brain injury. The disorder is treated with a prophylactic
CC agent which increases the permeability of the blood/brain barrier, or
CC with an anticoagulant and a secondary agent selected from bradykinin,
CC serotonin, histamine and arachidonic acid. The agent is a purified
CC UCP-2 polypeptide in combination with an anticoagulant. The method is
CC also useful for screening for an agent useful for treating a neurological
CC disorder or a neuronal injury. The present sequence represents the
CC coding sequence of human UCP-2, the gene of which is located on
CC chromosome 11.
XX
SQ Sequence 930 BP; 185 A; 285 C; 255 G; 205 T; 0 other;
XX
Query Match 99.8%; Score 928.4; DB 24; Length 930;
Best Local Similarity 99.9%; Pred. No. 9.7e-239;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
DB 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
QY 61 GGCACAGCTGCTGTCATCGCATATCTACACCTTCTCTTGGAATCTGTAAGTCCGG 120
DB 61 GGCACAGCTGCTGTCATCGCATATCTACACCTTCTCTTGGAATCTGTAAGTCCGG 120
QY 121 TTACAGATCCCAAGAGAAAGTCAAGGGCCAGTCCGGCTACAGCAGGCGCCAGTACCGC 180
DB 121 TTACAGATCCCAAGAGAAAGTCAAGGGCCAGTCCGGCTACAGCAGGCGCCAGTACCGC 180

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DB 121 TTACAGATCCAGGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCGACGTAACCG 180
 QY 181 GGTGATGAGGACCACTCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 GGTGATGAGGACCACTCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 GGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 GGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 GATTCGTCAACAGTCTTACACCAAGGGCTCTGAGCATGACCATTTGGAGAGCCGCTC 360
 DB 301 GATTCGTCAACAGTCTTACACCAAGGGCTCTGAGCATGACCATTTGGAGAGCCGCTC 360
 QY 361 CTAGCAGAGCAGCAGCAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 CTAGCAGAGCAGCAGCAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 AAGTCCGATTCGACAGCTCAGGCGCGGCTGAGAGTGTGAGATACCAAGACCGCTC 480
 DB 421 AAGTCCGATTCGACAGCTCAGGCGCGGCTGAGAGTGTGAGATACCAAGACCGCTC 480
 QY 481 AATGCTACAGACCACTTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 481 AATGCTACAGACCACTTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 CCCAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 CCCAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 601 AAGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 601 AAGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 661 GCGTTGGGGGAGGCTTCTGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 661 GCGTTGGGGGAGGCTTCTGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 721 AGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 AGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 CTCCAG 840
 DB 781 CTCCAG 840
 QY 841 GGTTCCTGAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 GGTTCCTGAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 GCGTGCATCTCCGAGAGAGGCTCCCTTCTGA 930
 DB 901 GCGTGCATCTCCGAGAGAGGCTCCCTTCTGA 930
 RESULT 11
 ID AAV82381 standard; DNA; 1596 BP.
 XX AAV82381;
 AC 31-MAR-1999 (first entry)
 DE Full length human C5 nucleotide sequence.
 KW Body weight disorder; obesity; appetite regulation; thermoregulation;
 KW anorexia; abnormal food intake; cachexia; thermogenesis; ss.
 OS Homo sapiens.
 XX US5853975-A.
 XX 29-DEC-1998.
 PD

XX 26-FEB-1997; 97US-0807861.
 PF 26-FEB-1997; 97US-0807861.
 XX 26-FEB-1997; 97US-0807861.
 PR 23-AUG-1994; 94US-0284522.
 PR 06-JUN-1995; 95US-0470868.
 PR 23-AUG-1995; 95US-0518878.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Tartaglia LA;
 PI WPI: 1999-094892/08.
 DR P-PDEB; AAM89546.
 XX Identifying modulators of C5 protein uncoupling activity - used as
 PT potential regulators of thermogenesis, appetite and body weight,
 PT e.g. for treating obesity, anorexia and cachexia
 XX Example: Fig 18; 83bp; English.
 PS The present invention describes a method for identifying a compound (I)
 CC that modulates C5 protein uncoupling activity by: (a) treating a test
 CC compound with C5 or cells expressing it; (b) measuring the level of
 CC uncoupling activity; and (c) comparing this with level of activity in
 CC the absence of the test compound. Any difference in the levels indicates
 CC a modulator. C5 protein has uncoupling activity, i.e. it can transport
 CC protons across the mitochondrial inner membrane, reducing the proton
 CC motive force and allowing dissipation of caloric energy as heat. It is
 CC thus a regulator of thermogenesis and is involved in body weight
 CC regulation. (I) are potentially useful in treatment of body weight
 CC disorders, regulation of appetite and thermoregulation, e.g. in cases of
 CC obesity, anorexia, abnormal food intake and cachexia. The present
 CC sequence represents the full length human C5 nucleotide sequence, from
 CC the present invention.
 SQ Sequence 1596 BP; 319 A; 506 C; 384 G; 387 T; 0 other;
 Query Match 99.8%; Score 928.4; DB 20; Length 1596;
 Best Local Similarity 99.9%; Pred. No. 1.2e-238;
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGTTGGGTTCAAGGCGACAGATGAGGCGGCTGACGCTGATGATGATGATGATGATGATGAT 60
 DB 313 ATGTTGGGTTCAAGGCGACAGATGAGGCGGCTGACGCTGATGATGATGATGATGATGATGAT 372
 QY 61 GGCACAGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 DB 373 GGCACAGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
 QY 121 TTACAGATCCAGAGAGAAAGTCAAGGGCCAGTGGGCTGACAGCCGCGAGTACCGG 180
 DB 433 TTACAGATCCAGAGAGAAAGTCAAGGGCCAGTGGGCTGACAGCCGCGAGTACCGG 492
 QY 181 GGTGATGAGGACCACTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 493 GGTGATGAGGACCACTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
 QY 241 GGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 553 GGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 612
 QY 301 GATTCGTCAACAGTCTTACACCAAGGGCTCTGAGCATGACCATTTGGAGAGCCGCTC 360
 DB 613 GATTCGTCAACAGTCTTACACCAAGGGCTCTGAGCATGACCATTTGGAGAGCCGCTC 672
 QY 361 CTAGCAGCAGCAGCAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 673 CTAGCAGCAGCAGCAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
 QY 421 AAGTCCGATTCGACAGCTCAGGCGCGGCTGAGAGTGTGAGATACCAAGACCGCTC 480
 DB 733 AAGTCCGATTCGACAGCTCAGGCGCGGCTGAGAGTGTGAGATACCAAGACCGCTC 792

QY 481 AATGCTACAAAGCAATTCGCCGAGAGAGAGGCTTCGAGGCGCTCTGGAAAGGAGACCTCT 540
 Db 793 AATGCTACAAAGCAATTCGCCGAGAGAGAGGCTTCGAGGCGCTCTGGAAAGGAGACCTCT 852
 QY 541 CCCAATGTTGCTGTATGATGCAATGTCACATGTCGTGAGCTGTGACCTATGACCTATC 600
 Db 853 CCCAATGTTGCTGTATGATGCAATGTCACATGTCGTGAGCTGTGACCTATGACCTATC 912
 QY 601 AACGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTGTCACCTTACCTCT 660
 Db 913 AAGGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTGTCACCTTACCTCT 972
 QY 661 GCCTTTGGGCGAGGCTTTGCAACAATGTCATGCTCCCTGTCAGAGCTGTGACAGAG 720
 Db 973 GCCTTTGGGCGAGGCTTTGCAACAATGTCATGCTCCCTGTCAGAGCTGTGACAGAG 1032
 QY 721 AGATACATGAATCTGCTGCGCCAGTACAGTACAGCTGCGCCATGTCCTTACCATG 780
 Db 1033 AGATACATGAATCTGCTGCGCCAGTACAGTACAGCTGCGCCATGTCCTTACCATG 1092
 QY 781 CTCGAGAGAGAGGAGGCGCCGAGGCTCTCAAAAGGATTCATGCTCCCTTCTCCGCTTG 840
 Db 1093 CTCGAGAGAGAGGAGGCGCCGAGGCTCTCAAAAGGATTCATGCTCCCTTCTCCGCTTG 1152
 QY 841 GGTTCCTGGAAGCTGTGATGTTGTCACCTATGAGCAGCTGAAACGAGCCTCATGCT 900
 Db 1153 GGTTCCTGGAAGCTGTGATGTTGTCACCTATGAGCAGCTGAAACGAGCCTCATGCT 1212
 QY 901 GCGTGCACCTCCCGAGAGGCTCCCTCTGA 930
 Db 1213 GCGTGCACCTCCCGAGAGGCTCCCTCTGA 1242

RESULT 12

AAA9716
 ID AAA9716 standard; cDNA; 1596 BP.

AAA9716;

06-FEB-2001 (first entry)

Mouse body weight-related cDNA SEQ ID NO: 38.

Mouse; body weight; immunomodulator; anorectic; obesity; cachexia;

thermogenesis; appetite; ss.

Mus sp.

US6121017-A.

19-SEP-2000.

08-OCT-1997; 97US-0946719.

26-FEB-1997; 97US-0807861.

23-AUG-1994; 94US-0294522.

06-JUN-1995; 95US-0470868.

23-AUG-1995; 95US-0518876.

(MILL-) MILENNTUM PHARM INC.

Tatrasila LA;

WPI; 2000-618197/59.

P-PSDB; AAB27018.

New human C5 gene and gene product, useful in regulating mammalian body weight and modulating thermogenesis, especially useful for treating body weight disorders, e.g., obesity or cachexia -

Claim 3; Fig 18; 84pp; English.

CC The present sequence is differentially expressed in body weight disorder
 CC states. It may be useful in modulating processes relating to mammalian
 CC body weight regulation, including treatment of body weight disorders,
 CC e.g. obesity or cachexia, and modulation of thermogenesis. It is also
 CC useful in regulating appetite and/or body weight. Furthermore, it is
 CC useful for diagnostic evaluation and prognosis of various body weight
 CC disorders, and for identifying subjects exhibiting a predisposition to
 CC such conditions.
 XX

Sequence 1596 BP; 319 A; 506 C; 384 G; 387 T; 0 other;

Query Match 99.8%; Score 928.4; DB 21; Length 1596;
 Best Local Similarity 99.9%; Pred. No. 1.2e-238;
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGCTGAGTTCAAGGCCAAGATGTCCTCCCTTACTGCACTGTGAAGTTCTTGGGCT 60
 Db 313 AATGCTGAGTTCAAGGCCAAGATGTCCTCCCTTACTGCACTGTGAAGTTCTTGGGCT 372
 QY 61 GGCACAGCTGCTGATGCAATCTCATACCTTCTCTGATGCTGTAAGTCGG 120
 Db 373 GGCACAGCTGCTGATGCAATCTCATACCTTCTCTGATGCTGTAAGTCGG 432
 QY 121 TTACAGATCCAAAGAAAGTCAAGGCGCAGTGCCTGCTACAGCCAGCCAGTACCG 180
 Db 433 TTACAGATCCAAAGAAAGTCAAGGCGCAGTGCCTGCTACAGCCAGCCAGTACCG 492
 QY 181 GGTGTGATGAGCAATCTGATGCAATGCTGTACTAGAGGCCCCGGAAGCTTACAT 240
 Db 493 GGTGTGATGAGCAATCTGATGCAATGCTGTACTAGAGGCCCCGGAAGCTTACAT 552
 QY 241 GGGCTGTTGCCGCGCTGAGGCGCAATGAGCTTGTGCTGTCCGATGCGCTGAT 300
 Db 553 GGGCTGTTGCCGCGCTGAGGCGCAATGAGCTTGTGCTGTCCGATGCGCTGAT 612
 QY 301 GATTCTGCAAAAGTTCTACACCAAGGCTCTGACATGTCAGATTTGGAGCGGCTC 360
 Db 613 GATTCTGCAAAAGTTCTACACCAAGGCTCTGACATGTCAGATTTGGAGCGGCTC 672
 QY 361 CTAGCAGGAGACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 673 CTAGCAGGAGACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
 QY 421 AAGTCCGATTCGAACTCAGGCGCGGCTGAGGTGTGAGATACCAAGCAAGCTC 480
 Db 733 AAGTCCGATTCGAACTCAGGCGCGGCTGAGGTGTGAGATACCAAGCAAGCTC 792
 QY 481 AATGCTACAAAGCAATTCGCGGAGAGAAAGGATTCGCGGCGCTCTGAAAGGAGCTCT 540
 Db 793 AATGCTACAAAGCAATTCGCGGAGAGAAAGGATTCGCGGCGCTCTGAAAGGAGCTCT 852
 QY 541 CCCAATGTTGCTGTATGATGCAATGTCATGTCGTGAGCTGTGACCTATGACCTATC 600
 Db 853 CCCAATGTTGCTGTATGATGCAATGTCATGTCGTGAGCTGTGACCTATGACCTATC 912
 QY 601 AAGGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTGTCACCTTACCTCT 660
 Db 913 AAGGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTGTCACCTTACCTCT 972
 QY 661 GCCTTTGGGCGAGGCTTTGCAACAATGTCATGCTCCCTGTCAGAGCTGTGACAGAG 720
 Db 973 GCCTTTGGGCGAGGCTTTGCAACAATGTCATGCTCCCTGTCAGAGCTGTGACAGAG 1032
 QY 721 AGATACATGAATCTGCTGCGCCAGTACAGTACAGCTGCGCCATGTCCTTACCATG 780
 Db 1033 AGATACATGAATCTGCTGCGCCAGTACAGTACAGCTGCGCCATGTCCTTACCATG 1092
 QY 781 CTCGAGAGAGAGGAGGCGCCGAGGCTCTCAAAAGGATTCATGCTCCCTTCTCCGCTTG 840
 Db 1093 CTCGAGAGAGAGGAGGCGCCGAGGCTCTCAAAAGGATTCATGCTCCCTTCTCCGCTTG 1152
 QY 841 GGTTCCTGGAAGCTGTGATGTTGTCACCTATGAGCAGCTGAAACGAGCCTCATGCT 900


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QY 541 CCATGTTGCTCGAATGCAATGCTGAGTGGTGAACCTATGACTCATC 600
DB 885 CCAATGTTGCTCGAATGCAATGCTGAGTGGTGAACCTATGACTCATC 944
QY 601 AAGATGCTCTCTGAAAGCACTCATGACAGATGACCTCTGCACTTCT 660
DB 945 AAGATGCTCTCTGAAAGCACTCATGACAGATGACCTCTGCACTTCT 1004
QY 661 GCCTTTGGGAGGCTTCTGACACCTGATGCTGCTGCTGCTGCTGCTG 720
DB 1005 GCCTTTGGGAGGCTTCTGACACCTGATGCTGCTGCTGCTGCTGCTG 1064
QY 721 AGATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 1065 AGATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
QY 781 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 1125 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1184
QY 841 GGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 1185 GGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1244
QY 901 GCCTGCACTTCCCGAGAGGCTCTCTTCTGA 930
DB 1245 GCCTGCACTTCCCGAGAGGCTCTCTTCTGA 1274

```

RESULT 15

AA229244
ID AA229244 standard; cDNA; 1882 BP.

AA229244;

28-FEB-2000 (first entry)

Human mitochondrial anion carrier, uncoupling protein-2 cDNA.

XX Mitochondrial uncoupling protein-2; UCP-2; mitochondrial anion carrier;
 XX MAC; modulator; transport protein; fatty acid anion; mitochondria;
 XX assay vesicle; metabolic disorder; diabetes; obesity; cancer; human; ds.
 OS Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 315..1244
 XX FT /*tag= a
 XX FT /product= "UCP-2"

PN W09964458-A1.

PD 16-DEC-1999.

XX 08-JUN-1999; 99WO-US12623.

XX 08-JUN-1998; 98US-0093662.

PA (UYBO-) UNIV BOSTON.

XX Corkey BE, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;

DR WPI; 2000-087200/07.

XX P-PSDB; AAY44252.

PT Identifying modulators of mitochondrial anion carriers, potentially
 XX useful for treating metabolic disease, e.g. diabetes and obesity

XX Claim 11; Pages 69-70; 80pp; English.

CC The present sequence is a cDNA encoding human uncoupling protein-2
 CC (UCP-2) which is a mitochondrial anion carrier (MAC). The UCPs transport
 CC free fatty acid anions across the inner mitochondrial membrane to induce

CC cyclical proton movement. This transport is tightly related to oxidation
 CC of fatty acids in the mitochondria, thereby converting fatty acids into
 CC energy rather than storing them. The uncoupling protein is used in the
 CC preparation of assay vesicles that are used to identify modulators of
 CC MAC activity. MAC modulators are useful for treating metabolic disorders,
 CC particularly diabetes and obesity. Modulators that act as inhibitors
 CC can be used to treat conditions requiring a reduction in energy
 CC expenditure, e.g. in cancer patients or the elderly.

XX Sequence 1882 BP; 371 A; 599 C; 464 G; 448 T; 0 other;

Query Match 99.8%; Score 928.4; DB 21; Length 1882;

Best Local Similarity 99.8%; Pred. No. 1.2e-238;

Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 315 ATGGTGGGTTCAAGGCAAGATGAGGCGCCCTGCTGCTGCTGCTGCTGCTG 374
QY 61 GGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 375 GGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 434
QY 121 TTACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 435 TTACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494
QY 181 GGTGTGATGAGGCAACATTTGACATGATGATGATGATGATGATGATGATGAT 240
DB 495 GGTGTGATGAGGCAACATTTGACATGATGATGATGATGATGATGATGATGAT 554
QY 241 GGGCTGTTGCGCGGCTGCGAGCGCGCAAGAGAGAGAGAGAGAGAGAGAG 300
DB 555 GGGCTGTTGCGCGGCTGCGAGCGCGCAAGAGAGAGAGAGAGAGAGAGAG 614
QY 301 GATTCTGTCAAAAGATTCTACACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 615 GATTCTGTCAAAAGATTCTACACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 674
QY 361 CTACAGAGCAGACACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 675 CTACAGAGCAGACACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
QY 421 AAGTTCGATTCAGAGCTCAGAGCGCGGCTGAGAGAGAGAGAGAGAGAGAG 480
DB 735 AAGTTCGATTCAGAGCTCAGAGCGCGGCTGAGAGAGAGAGAGAGAGAGAG 794
QY 481 AATGCTTCAAAAGACATTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 795 AATGCTTCAAAAGACATTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
QY 541 CCCAATGTGCTGTAATGCAATGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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QY 601 AAGATGCTCTCTGAAAGCACTCATGACAGATGACCTCTTGCACCTTCT 660
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QY 661 GCCTTTGGGAGGCTTCTGACACCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 720
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QY 781 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 1095 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1154
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Qy	901	GCCTGCACTTCCCGAGAGGCTCCCTTCTGA	930
Db	1215	GCCTGCACTTCCCGAGAGGCTCCCTTCTGA	1244

Search completed: February 4, 2004, 18:26:04
Job time : 315 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 18:07:02 ; Search time 75 Seconds

(without alignments)
5473.151 Million cell updates/sec

Title: US-09-884-814-2

Perfect score: 930
Sequence: 1 atcggttgaggtcgaagccac.....cccgagagctccctctga 930

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/prodata/1/ina/PCUTS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	928.4	99.8	1536	2 US-08-807-861A-38	Sequence 38, Appl
2	928.4	99.8	1536	3 US-09-210-681-38	Sequence 38, Appl
3	928.4	99.8	1536	3 US-08-946-719A-38	Sequence 38, Appl
4	928.4	99.8	1536	4 US-09-547-983-38	Sequence 38, Appl
5	888.4	96.6	1255	1 US-08-518-878B-38	Sequence 38, Appl
6	888.4	96.6	1255	1 US-08-294-522B-38	Sequence 38, Appl
7	888.4	96.6	1255	2 US-08-470-868A-38	Sequence 38, Appl
8	888.4	96.6	1255	1 US-08-518-878B-38	Sequence 36, Appl
9	618	66.5	1205	1 US-08-294-522B-37	Sequence 37, Appl
10	618	66.5	1205	2 US-08-807-861A-36	Sequence 36, Appl
11	618	66.5	1205	2 US-08-470-868A-36	Sequence 36, Appl
12	618	66.5	1205	3 US-09-210-681-36	Sequence 36, Appl
13	618	66.5	1205	4 US-08-946-719A-36	Sequence 36, Appl
14	618	66.5	1205	4 US-09-547-983-36	Sequence 36, Appl
15	508.8	54.7	512	4 US-09-702-705-1014	Sequence 1014, Ap
16	508.8	54.7	512	4 US-09-736-457-1014	Sequence 1014, Ap
17	472.4	50.8	1192	3 US-09-142-565-1	Sequence 1, Appl
18	471.8	50.7	2782	2 US-08-937-466-1	Sequence 1, Appl
19	471.8	50.7	2782	2 US-09-172-528-1	Sequence 1, Appl
20	471.8	50.7	2782	3 US-09-318-199-1	Sequence 1, Appl
21	471.8	50.7	2782	3 US-09-503-579-1	Sequence 1, Appl
22	469.2	50.5	1949	2 US-08-937-466-3	Sequence 3, Appl
23	469.2	50.5	1949	2 US-09-172-528-3	Sequence 3, Appl
24	469.2	50.5	1949	3 US-09-318-199-3	Sequence 3, Appl
25	469.2	50.5	1949	3 US-09-503-579-3	Sequence 3, Appl
26	390.6	42.0	1777	2 US-08-937-466-5	Sequence 5, Appl
27	390.6	42.0	1777	2 US-08-172-528-5	Sequence 5, Appl

28	390.6	42.0	1777	3 US-09-318-199-5	Sequence 5, Appl
29	390.6	42.0	1777	3 US-09-503-579-5	Sequence 5, Appl
30	316.4	34.0	318	4 US-09-702-705-1376	Sequence 1376, Ap
31	316.4	34.0	318	4 US-09-736-457-1376	Sequence 1376, Ap
32	241.8	26.0	309	1 US-08-518-878B-14	Sequence 14, Appl
33	241.8	26.0	309	1 US-08-294-522B-14	Sequence 14, Appl
34	241.8	26.0	309	2 US-08-807-861A-14	Sequence 14, Appl
35	241.8	26.0	309	2 US-08-470-868A-14	Sequence 14, Appl
36	241.8	26.0	309	3 US-09-210-681-14	Sequence 14, Appl
37	241.8	26.0	309	3 US-08-946-719A-14	Sequence 14, Appl
38	241.8	26.0	309	4 US-09-547-983-14	Sequence 14, Appl
39	178.6	19.2	847	3 US-09-142-565-5	Sequence 5, Appl
40	111.6	12.0	309	1 US-08-518-878B-15	Sequence 15, Appl
41	111.6	12.0	309	1 US-08-294-522B-15	Sequence 15, Appl
42	111.6	12.0	309	2 US-08-807-861A-15	Sequence 15, Appl
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44	111.6	12.0	309	3 US-09-210-681-15	Sequence 15, Appl
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ALIGNMENTS

RESULT 1
US-08-807-861A-38
Sequence 38, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Targadia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/254,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-807-861A-38
Query Match 99.8%; Score 928.4; DB 2; Length 1536;

Best Local Similarity 99.9%; Pred. No. 7.9e-242;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGTGGGTTCAAGGCCACAGATGTGCCCCCTTACTGCTGAAAGTTTCTTGGGGCT 60
Db 313 ATGGTGGGTTCAAGGCCACAGATGTGCCCCCTTACTGCTGAAAGTTTCTTGGGGCT 372
QY 61 GGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 373 GGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
QY 121 TTACAGATCCAAAGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 433 TTACAGATCCAAAGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
QY 181 GGTGTGATGGGACCATTCATGACATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 493 GGTGTGATGGGACCATTCATGACATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 241 GGGCTGTGTCGGGCTGACAGCGCCAAATGAGCTTTGCTGTGCTGATGAGCTGTAT 300
Db 553 GGGCTGTGTCGGGCTGACAGCGCCAAATGAGCTTTGCTGTGCTGATGAGCTGTAT 612
QY 301 GATTGTGCAAAAGTTTCTACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 613 GATTGTGCAAAAGTTTCTACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 672
QY 361 CTAGCAGGACAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 673 CTAGCAGGACAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
QY 421 AAGGTCCGATTCAGAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 733 AAGGTCCGATTCAGAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792
QY 481 AATGCTTCAAGACCATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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QY 541 CCCAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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Db 913 AAGGATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972
QY 661 GCGTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
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Db 1093 CTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1152
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Db 1153 GGTTCCTGGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1212
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RESULT 2
US-09-210-681-38
Sequence 38, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:

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: APPLICANT: Tartaglia, Louis A.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
: TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESS: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/210,681
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/807,861
: FILING DATE: 26-FEB-1997
: APPLICATION NUMBER: US 08/518,878
: FILING DATE: 23-AUG-1995
: APPLICATION NUMBER: US 08/470,868
: FILING DATE: 06-JUN-1995
: APPLICATION NUMBER: US 08/294,522
: FILING DATE: 23-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7853-066
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 38:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1596 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-09-210-681-38
:
: Query Match: 99.8%; Score 928.4; DB 3; Length 1596;
: Best Local Similarity 99.9%; Pred. No. 7.9e-242;
: Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY		361	CTAGACGCGACACCA	CAGGTGCCCTTGGCTGTGGCTGTGGCCCAAGCCACGGATGTGGTA	420
Db		673	CTAGAGAGGACACACA	CAGGTGCCCTTGGCTGTGGCTGTGGCCCAAGCCACGGATGTGGTA	732
QY		421	AAGGTCCGATTCCA	AGTCAGAGCCCCGGCTGAGAGTGTCGGAAGATACCAAAGAACCCTC	480
Db		733	AAGGTCCGATTCCA	AGTCAGAGCCCCGGCTGAGAGTGTCGGAAGATACCAAAGAACCCTC	792
QY		481	AATGCCCTACAGAAC	CATTTGCCCGAGAGAAAGGTTCCGGGGCCCTCTGAAAAGGACTCT	540
Db		793	AATGCCCTACAGAAC	CATTTGCCCGAGAGAAAGGTTCCGGGGCCCTCTGAAAAGGACTCT	852
QY		541	CCCAATGTTGCCTG	TAATGAGCATTTGTAACTGTGACTGAGTGGTAGCCATGACCTCATC	600
Db		853	CCCAATGTTGCCTG	TAATGAGCATTTGTAACTGTGACTGAGTGGTAGCCATGACCTCATC	912
QY		601	AAGGATGCCCTCTG	AAAAAGCCAACTCATGACAGATGACCTCCCTTGCCACTTCATTTCT	660
Db		913	AAGGATGCCCTCTG	AAAAAGCCAACTCATGACAGATGACCTCCCTTGCCACTTCATTTCT	972
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Db		973	GCCCTTGGGGGAGG	CTTTGACACACATGTATGGCTCCCTGTAAGCTGTGTAAGAGG	1032
QY		721	AGATACATATACTG	CGCCTGTGAGCAGTACAGTACGCTGGCCACTGTGCCCCTTACATG	780
Db		1033	AGATACATATACTG	CGCCTGTGAGCAGTACAGTACGCTGGCCACTGTGCCCCTTACATG	1092
QY		781	CTCCAGAAAGAGAGG	CCCCGAGCCTTTCTACAAAGGGTTATGCCCCCTTTCCGCTTG	840
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QY		841	GGTTCCTGGAAGST	GTATGTGCTCACCTATAGACAGCTGAACGACCCTCATGTGCT	900
Db		1153	GGTTCCTGGAAGST	GTATGTGCTCACCTATAGACAGCTGAACGACCCTCATGTGCT	1212
QY		901	GCCTGCACCTCCG	AGAGGCTTCCTTTCTGA	930
Db		1213	GCCTGCACCTCCG	AGAGGCTTCCTTTCTGA	1242

RESULT 3
US-08-946-719A-38
Sequence 38, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edwards LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868

```

FLYING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-946-719A-38

Query Match          99.8%; Score 928.4; DB 3; Length 1596;
Best Local Similarity 99.9%; Pred. No. 7.9e+242;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGCTTGGGCTTCAGGCCACAGATGTGCCCCCTACTCTGCCACTGTGAAGTTCTTGGGGCT 60
DB      313  ATGGTTGGGTTTCAGGGCCACAGATGTGCCCCCTACTCTGCCACTGTGAAGTTCTTGGGGCT 372

QY      61  GGCACAGCTGCTGTCATGCGAGATCTCATCACTTTCTCTGSAATACTGCTAAAGTCCGG 120
DB      373  GGCACAGCTGCTGTCATGCGAGATCTCATCACTTTCTCTGSAATACTGCTAAAGTCCGG 432

QY      121  TTACAGATCCAGAGAAAGTCAAGGGCCATGTGCGCGCTACAGCCAGCCGCGCATGATCCGC 180
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QY      181  GGTGTGATGGGACCATCTTGACCATGTGCTACTAGAGGGCCCCCGAAGCCTTCAACAT 240
DB      493  GGTGTGATGGGACCATCTTGACCATGTGCTACTAGAGGGCCCCCGAAGCCTTCAACAT 552

QY      241  GGGCTGATTGCCGCGCTTGACGCGCAAAATGAGCTTTGCTGTGCGCATCGGCTGTAT 300
DB      553  GGGCTGATTGCCGCGCTTGACGCGCAAAATGAGCTTTGCTGTGCGCATCGGCTGTAT 612

QY      301  GATTCTGTCAACAGTTTCTACCAAGGCGCTGAGAGTCCAGACATTGGGAGCGCGCTC 360
DB      613  GATTCTGTCAACAGTTTCTACCAAGGCGCTGAGAGTCCAGACATTGGGAGCGCGCTC 672

QY      361  CTAGCAGGACGACCAAGTGGGCTGTGAGCTGTGGCTGTGGCCAGCCACGGATGTGTA 420
DB      673  CTAGCAGGACGACCAAGTGGGCTGTGAGCTGTGGCTGTGGCCAGCCACGGATGTGTA 732

QY      421  AAGGTCGATTCGAAGCTCAGGCCCCGGGCTGAGAGTGTGCGAGATACCAAGACGCCGC 480
DB      733  AAGGTCGATTCGAAGCTCAGGCCCCGGGCTGAGAGTGTGCGAGATACCAAGACGCCGC 792

QY      481  AATGCTCAACAACCATTTGCCAGAGAGAAAGGTTCCGGGGCCTCTGGAAGAGGACCTCT 540
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DB      853  CCCAATGTGTCTGTAAATGCAATGTGTCACTGTGCTGAGTGGGTGACCTATGACCTCATC 912

QY      601  AAGGATGCGCTCTGTAAGACCAACCTCATGACAGATGACCTCCCTTGGCACTTCACTTCT 660
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QY      661  GCGTTTGGGAGCGCTTCTGACACCACTGTCACTGCGCTCCCTGTAAAGCTGGTCAAAGAC 720
DB      973  GCGTTTGGGAGCGCTTCTGACACCACTGTCACTGCGCTCCCTGTAAAGCTGGTCAAAGAC 1032

QY      721  AGATTAAATGAATCTGCGCCTGGGCGCAGTACAGTACGCTGGCACTGTGCGCTTACATG 780

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Db 1033 AGATCATGAACCTCTGCGCTGGGCGAGTACAGTACCGCTGCGCACTGTGCTTACCATG 1092
Qy 781 CTCGAGAGAGAGGGGCCCCGAGCCTTCTACAAAGGTTCAATGCGCTTCTTCTCGCTTG 840
Db 1093 CTCGAGAGAGAGGGGCCCCGAGCCTTCTACAAAGGTTCAATGCGCTTCTTCTCGCTTG 1152
Qy 841 GGTTCCTGGAAGGTGATGATGCTGACCTATGAGCAGCTGAAGAGCGCTCATGGCT 900
Db 1153 GGTTCCTGGAAGGTGATGATGCTGACCTATGAGCAGCTGAAGAGCGCTCATGGCT 1212
Qy 901 GCTGCACTTCCCGAGAGGCTTCTTCTGA 930
Db 1213 GCTGCACTTCCCGAGAGGCTTCTTCTGA 1242

RESULT 4
US-09-547-983-38
; Sequence 38, Application US/09547983
; Patent No. 6518402
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,983
; FILING DATE: 12-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1596 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-547-983-38.

Query Match 99.8%; Score 928.4; DB 4; Length 1596;
Best Local Similarity 99.9%; Pred. No. 7.9e-242;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGTTGGTTCAAGGCCACAGATGTCCTACTGCACTGTGAAGTTTCTTGGGGCT 60

Db 313 ATGGTTGGTTCAAGGCCACAGATGTCCTACTGCACTGTGAAGTTTCTTGGGGCT 372
Qy 61 GGCACAGCTCCGTCAGATTCGACATCACTTCCCTGAGATACGCTTAAGTCGG 120
Db 373 GGCACAGCTCCGTCAGATTCGACATCACTTCCCTGAGATACGCTTAAGTCGG 432
Qy 121 TTACAGATCCAGAGAGAAAGTCAAGGGCCAGTGCCTGACAGCCAGCCAGTAACGC 180
Db 433 TTACAGATCCAGAGAGAAAGTCAAGGGCCAGTGCCTGACAGCCAGCCAGTAACGC 492
Qy 181 GGTGTATGAGGACATTTGACACATGATGCTGATGAGGCGCCCGAAGCCTTACAT 240
Db 493 GGTGTATGAGGACATTTGACACATGATGCTGATGAGGCGCCCGAAGCCTTACAT 552
Qy 241 GGGCTGTTCCGGGCTGACAGCGCCAAATGAGCTTCTGTCGATCGAGCTGTAT 300
Db 553 GGGCTGTTCCGGGCTGACAGCGCCAAATGAGCTTCTGTCGATCGAGCTGTAT 612
Qy 301 GATTCTGCAACAGTTCTTACACAAAGGCTCTGACATGCAAGCTTTGGAGCGGCTTC 360
Db 613 GATTCTGCAACAGTTCTTACACAAAGGCTCTGACATGCAAGCTTTGGAGCGGCTTC 672
Qy 361 CTACAGAGCAGACACAGAGTGCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 673 CTACAGAGCAGACACAGAGTGCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 732
Qy 421 AAGTCCGATTCAGAGCTCAGGCTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 733 AAGTCCGATTCAGAGCTCAGGCTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 792
Qy 481 AATGCTCAACAGACATTCGCGGAGAGAAAGGTTCCGGGCTCTGAAAGGACCTCT 540
Db 793 AATGCTCAACAGACATTCGCGGAGAGAAAGGTTCCGGGCTCTGAAAGGACCTCT 852
Qy 541 CCAATGTTGCTGTAATGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCT 600
Db 853 CCAATGTTGCTGTAATGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCT 912
Qy 601 AAGATGCGCTCTGAAAGGCAACCTCATGACAGATGACCTCCCTGCACTTCACTTCT 660
Db 913 AAGATGCGCTCTGAAAGGCAACCTCATGACAGATGACCTCCCTGCACTTCACTTCT 972
Qy 661 GCTTTGGAGGAGGCTTCTGACCACTGTATGCTGCTTCTGTAAGCTGTGAAGAG 720
Db 973 GCTTTGGAGGAGGCTTCTGACCACTGTATGCTGCTTCTGTAAGCTGTGAAGAG 1032
Qy 721 AGATCATGAACCTGCGCTGAGGCGAGTACAGTACAGTACAGTACAGTACAGTACAG 780
Db 1033 AGATCATGAACCTGCGCTGAGGCGAGTACAGTACAGTACAGTACAGTACAGTACAG 1092
Qy 781 CTCGAGAGAGAGGGGCCCCGAGCCTTCTACAAAGGTTCAATGCGCTTCTTCTCGCTTG 840
Db 1093 CTCGAGAGAGAGGGGCCCCGAGCCTTCTACAAAGGTTCAATGCGCTTCTTCTCGCTTG 1152
Qy 841 GGTTCCTGGAAGGTGATGATGCTGACCTATGAGCAGCTGAAGAGCGCTCATGGCT 900
Db 1153 GGTTCCTGGAAGGTGATGATGCTGACCTATGAGCAGCTGAAGAGCGCTCATGGCT 1212
Qy 901 GCTGCACTTCCCGAGAGGCTTCTTCTGA 930
Db 1213 GCTGCACTTCCCGAGAGGCTTCTTCTGA 1242

RESULT 5
US-08-518-878B-38
; Sequence 38, Application US/0851878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/518,878B
 FILING DATE: 23-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-036
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8664
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1255 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-518-878B-38

Query Match 96.6%; Score 898.4; DB 1; Length 1255;
 Best Local Similarity 99.9%; Pred. No. 9.5e-234;
 Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

31 CCTACGCACTGTGAAGTTCTTGGGGCTGCGACAGCTGCTGATCGAGATCTATC 90
 1 CCTACTGCCACTGTGAAGTTCTTGGGGCTGCGACAGCTGCTGATCGAGATCTATC 60
 91 ACCTTCTCTGTGATTAAGTCCGGTTACAGATCCAAAGGAAAGTCAGGGCCA 150
 61 ACCTTCTCTGTGATTAAGTCCGGTTACAGATCCAAAGGAAAGTCAGGGCCA 120
 151 GTGCGGCTACAGCCGCGCCAGTACCGCGGTGATGAGGGGACCATTTCTAGATG 210
 121 GTGCGGCTACAGTACGCGCCAGTACCGCGGTGATGAGGGGACCATTTCTAGATG 180
 211 CGTACTGAGGGGCCCCGGAAGCTCTCAATGAGGCTGTGCGCGCTGCAAGCCCAATG 270
 181 CGTACTGAGGGGCCCCGGAAGCTCTCAATGAGGCTGTGCGCGCTGCAAGCCCAATG 240
 271 AGCTTGTCTGTCTGCGCATCGGCTGTATGATTTCTGTCAACAGTTTCTACCAAGGCC 330
 241 AGCTTGTCTGTCTGCGCATCGGCTGTATGATTTCTGTCAACAGTTTCTACCAAGGCC 300
 331 TCTGAGCATGCGAGCATTTGGAGCGCGCTCTTACAGAGGACAGACAGAGTCCCTGCT 390
 301 TCTGAGCATGCGAGCATTTGGAGCGCGCTCTTACAGAGGACAGACAGAGTCCCTGCT 360
 391 GTGCGTGTGCGCCCAAGCCCAAGATGTGTAAGGTCCGATTCGAGCTCAGCGCGGCT 450
 361 GTGCGTGTGCGCCCAAGCCCAAGATGTGTAAGGTCCGATTCGAGCTCAGCGCGGCT 420
 451 GGAAGTGTGCGAGATACCAAGCAAGCTCAATGCTCAAGAGCATTTGCCGAGAGAA 510
 421 GGAAGTGTGCGAGATACCAAGCAAGCTCAATGCTCAAGAGCATTTGCCGAGAGAA 480
 511 GGGTTCCGGGGCTCTTGAAAGGAGCTTCCCAATGTTGCTGTATGCAATTTGTCAAC 570
 481 GGGTTCCGGGGCTCTTGAAAGGAGCTTCCCAATGTTGCTGTATGCAATTTGTCAAC 540
 571 TGTGCTGAGTGTGATGACTATGACTCATCAAGAGATGCCCTCTGAAAGCCAACTCATG 630

541 TGTGCTGAGTGTGATGACTATGACTCATCAAGAGATGCCCTCTGAAAGCCAACTCATG 600
 631 ACAGATGACCTCTCTTGGCACTTCTGCTTTGGGGGAGGCTTTGCAACCAATGTC 690
 601 ACAGATGACCTCTCTTGGCACTTCTGCTTTGGGGGAGGCTTTGCAACCAATGTC 660
 691 ATCCGCTCCCTGTAGACGTGTGCAAGACGATATACATGACTCTCCCTGGGCGAGTAC 750
 661 ATCCGCTCCCTGTAGACGTGTGCAAGACGATATACATGACTCTCCCTGGGCGAGTAC 720
 751 AGTACGCTGCGCACTGTGCTTACATGCTTCAAGAGAGGGGCGCCGAGCTTCTAC 810
 721 AGTACGCTGCGCACTGTGCTTACATGCTTCAAGAGAGGGGCGCCGAGCTTCTAC 780
 811 AAAGGTTGATGCGCTCTCTTCTCGGCTGGGTTCCGGAACGTGTGATGTTGTCACC 870
 781 AAAGGTTGATGCGCTCTCTTCTCGGCTGGGTTCCGGAACGTGTGATGTTGTCACC 840
 871 TATGACAGCTGAAAGAGAGCCCTGATGAGTGTGCTGCACTTCCGAGAGGCTCCCTTCTGA 930
 841 TATGACAGCTGAAAGAGAGCCCTGATGAGTGTGCTGCACTTCCGAGAGGCTCCCTTCTGA 900

RESULT 6

US-08-294-522B-38

Sequence 38, Application US/08294522B

Patent No. 5741666

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: Compositions and Methods for the

TITILE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,522B

FILING DATE: 23-AUG-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-015

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8664/9741

SEQUENCE CHARACTERISTICS:

LENGTH: 1255 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-294-522B-38

Query Match 96.6%; Score 898.4; DB 1; Length 1255;
 Best Local Similarity 99.9%; Pred. No. 9.5e-234;
 Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

31 CCTACGCACTGTGAAGTTCTTGGGGCTGCGACAGCTGCTGATCGAGATCTATC 90
 1 CCTACTGCCACTGTGAAGTTCTTGGGGCTGCGACAGCTGCTGATCGAGATCTATC 60
 91 ACCTTCTCTGTGATTAAGTCCGGTTACAGATCCAAAGGAAAGTCAGGGCCA 150


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Db      61  ACCCTTCCTGTGATCTGTCTAAAGTCCGGTTACAGATCCAGAGAAAGTCAAGGAGCA 120
Qy      151  GTGGCGCTACAGCCAGCCAGCCAGTACCGCGGTGTATGGGACACATTTCTGACATGGTG 210
Db      121  GTGGCGCTACAGCCAGCCAGCCAGTACCGCGGTGTATGGGACACATTTCTGACATGGTG 180
Qy      211  CGTACTAGAGGCCCCGAGAGGCTTCTACATAGGCTGTGGTCCGGCTGACAGGCCCAATG 270
Db      181  CGTACTAGAGGCCCCGAGAGGCTTCTACATAGGCTGTGGTCCGGCTGACAGGCCCAATG 240
Qy      271  AGCTTGGCTCTGTCGGCATGAGCTGTATGATTTGTCTAAACAGTTCTACACAGGSC 330
Db      241  AGCTTGGCTCTGTCGGCATGAGCTGTATGATTTGTCTAAACAGTTCTACACAGGSC 300
Qy      331  TCTGAGCATGCGACCATTTGGAGCGGCTCTCTAGACAGGACACACAGGTCCTGGCT 390
Db      301  TCTGAGCATGCGACCATTTGGAGCGGCTCTCTAGACAGGACACACAGGTCCTGGCT 360
Qy      391  GTGGCTGTGGCGCCAGCCAGGATGTGTAAAGTCCGATTCGACGTCAGGCGCGGCT 450
Db      361  GTGGCTGTGGCGCCAGCCAGGATGTGTAAAGTCCGATTCGACGTCAGGCGCGGCT 420
Qy      451  GAGGTGTCTCGAGATACCAAGACCGTCATGCTCTACAAACCAATTGCCGAGAGAA 510
Db      421  GAGGTGTCTCGAGATACCAAGACCGTCATGCTCTACAAACCAATTGCCGAGAGAA 480
Qy      511  GGGTTCCGGGGGCTCTGTGAAAGGAGCCTCTCCCATATGCTGTATGCAATTTGTCAAC 570
Db      481  GGGTTCCGGGGGCTCTGTGAAAGGAGCCTCTCCCATATGCTGTATGCAATTTGTCAAC 540
Qy      571  TGTGTGAGCTGTGACCTATGACCTCATCAAGAGATCCCTCTGAAAGCCACCTCATG 630
Db      541  TGTGTGAGCTGTGACCTATGACCTCATCAAGAGATCCCTCTGAAAGCCACCTCATG 600
Qy      631  ACAATGACCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 690
Db      601  ACAATGACCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 660
Qy      691  ATCGCTCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 750
Db      661  ATCGCTCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 720
Qy      751  AGTAGCGCTGCGCACTGTGCTTACCAATGCTCCAGAGAGAGGAGGCCCGACGCTTCTAC 780
Db      721  AGTAGCGCTGCGCACTGTGCTTACCAATGCTCCAGAGAGAGGAGGCCCGACGCTTCTAC 780
Qy      811  AAAGGTTTCAGTCCCTCTCTCTGCGCTTGGGTTCTGGAACGTGTGATGTCGTCAAC 870
Db      781  AAAGGTTTCAGTCCCTCTCTCTGCGCTTGGGTTCTGGAACGTGTGATGTCGTCAAC 840
Qy      871  TATGAGCAGCTGAAAGAGCCCTCATAGGCTGCTGCACTTCCGAGAGGCTCCCTTTCTGA 930
Db      841  TATGAGCAGCTGAAAGAGCCCTCATAGGCTGCTGCACTTCCGAGAGGCTCCCTTTCTGA 900

```

RESULT 7

US-08-470-868A-38
Sequence 38, Application US/08470868A

GENERAL INFORMATION:

APPLICANT: Targadia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITL OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8664
TELEX: 66441 PENNIE
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-38

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Query Match 96.6%; Score 898.4; DB 2; Length 1255;
Best Local Similarity 99.9%; Pred. No. 5,5e-234;
Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      31  CCTACTGCCACTGTGAAGTTCTCTGGGGCTGGGACAGCTGCTGCATGCAATCTCATC 90
Db      1  CCTACTGCCACTGTGAAGTTCTCTGGGGCTGGGACAGCTGCTGCATGCAATCTCATC 60
Qy      91  ACCTTCTCTGTGATCTGTCTAAAGTCCGTTACAGATCCAGAGAAAGTCAAGGGGCA 150
Db      61  ACCTTCTCTGTGATCTGTCTAAAGTCCGTTACAGATCCAGAGAAAGTCAAGGGGCA 120
Qy      151  GTGGCGCTACAGCCAGCCAGCCAGTACCGCGGTGTATGGGACACATTTCTGACATGGTG 210
Db      121  GTGGCGCTACAGCCAGCCAGCCAGTACCGCGGTGTATGGGACACATTTCTGACATGGTG 180
Qy      211  CGTACTAGAGGCCCCGAGAGGCTTCTACATAGGCTGTGGTCCGGCTGACAGGCCCAATG 270
Db      181  CGTACTAGAGGCCCCGAGAGGCTTCTACATAGGCTGTGGTCCGGCTGACAGGCCCAATG 240
Qy      271  AGCTTGGCTCTGTCGGCATGAGCTGTATGATTTGTCTAAACAGTTCTACACAGGSC 330
Db      241  AGCTTGGCTCTGTCGGCATGAGCTGTATGATTTGTCTAAACAGTTCTACACAGGSC 300
Qy      331  TCTGAGCATGCGACCATTTGGAGCGGCTCTCTAGACAGGACACACAGGTCCTGGCT 390
Db      301  TCTGAGCATGCGACCATTTGGAGCGGCTCTCTAGACAGGACACACAGGTCCTGGCT 360
Qy      391  GTGGCTGTGGCGCCAGCCAGGATGTGTAAAGTCCGATTCGACGTCAGGCGCGGCT 450
Db      361  GTGGCTGTGGCGCCAGCCAGGATGTGTAAAGTCCGATTCGACGTCAGGCGCGGCT 420
Qy      451  GAGGTGTCTCGAGATACCAAGACCGTCATGCTCTACAAACCAATTGCCGAGAGAA 510
Db      421  GAGGTGTCTCGAGATACCAAGACCGTCATGCTCTACAAACCAATTGCCGAGAGAA 480
Qy      511  GGGTTCCGGGGGCTCTGTGAAAGGAGCCTCTCCCATATGCTGTATGCAATTTGTCAAC 570
Db      481  GGGTTCCGGGGGCTCTGTGAAAGGAGCCTCTCCCATATGCTGTATGCAATTTGTCAAC 540
Qy      571  TGTGCTAGCTGTGATCTGACCTCATCAAGATCCCTCTGAAAGCCCAACCTCATG 630
Db      541  TGTGCTAGCTGTGATCTGACCTCATCAAGATCCCTCTGAAAGCCCAACCTCATG 600
Qy      631  ACAATGACCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 690
Db      601  ACAATGACCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 660
Qy      691  ATCGCTCTCTCTGTCACCTTCTGCACTTCTGCTTTGGGAGAGCTTTGCAACAATGTC 750

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Db 661 ATGCGCTCCCTGTAGAGCTGGTCAAGACAGATACATGAACCTGCGCTGGGCGAGTAC 720
 QY 751 AGTAGCGCTGGCCACTGTGCTTACATGCTCCAGAGAGAGGCCCCGAGCTTCTAC 810
 Db 721 AGTAGCGCTGGCCACTGTGCTTACATGCTCCAGAGAGAGGCCCCGAGCTTCTAC 780
 QY 811 AAGAGTTCAATGCGCTTCTTCCGCTTGGGTTCTGGAAGTGTGATGTTGTCACC 870
 Db 781 AAGAGTTCAATGCGCTTCTTCCGCTTGGGTTCTGGAAGTGTGATGTTGTCACC 840
 QY 871 TATGAGCAGCTGAAGACGCTTCATGCTGCTGCTGCACTTCCCGAGAGCTTCTTGA 930
 Db 841 TATGAGCAGCTGAAGACGCTTCATGCTGCTGCTGCACTTCCCGAGAGCTTCTTGA 900

RESULT 8

US-08-518-878B-36
 ; Sequence 36, Application US/0851878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/518,878B
 ; FILING DATE: 23-AUG-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-036
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1205 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-518-878B-36

Query Match 66.5%; Score 618; DB 1; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6.8e-158;
 Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

QY 1 ATGTTGGGTTCAAGGCCACAGATGTCCTTCTGGAATCTTCTTGGGCT 60
 Db 1 ATGTTGGGTTCAAGGCCACAGATGTCCTTCTGGAATCTTCTTGGGCT 60
 QY 61 GGCACAGCTGCTGATGAGCTGATCTACCTTCTGGAATCTTCTTGGGCT 120
 Db 61 GGCACAGCTGCTGATGAGCTGATCTACCTTCTGGAATCTTCTTGGGCT 120
 QY 121 TTACAGATCCAAAGGAGAAAGTCAAGGGGCGAGTGGCGCTTACAGCCGCTACCCG 180
 Db 121 TTACAGATCCAAAGGAGAAAGTCAAGGGGCGAGTGGCGCTTACAGCCGCTACCCG 180
 QY 181 GGTGTGATGGGACCATCTGACATGTTGTGCTAGTGAAGGGCCCCGGAAGCTCTACAT 240

Db 181 GGCCTTCTGGGATCCTTAACCATGATGAGGAGTCCACGACCTCTTCAAT 240
 QY 241 GGCCTTCTGGGATCCTTAACCATGATGAGGAGTCCACGACCTCTTCAAT 300
 Db 241 GGCCTTCTGGGATCCTTAACCATGATGAGGAGTCCACGACCTCTTCAAT 300
 QY 301 GATTCGTCAACAGTTCTTACACAGAGGCTCTAGCATGTCAGACATGGAAGCGCTC 360
 Db 301 GATTCGTCAACAGTTCTTACACAGAGGCTCTAGCATGTCAGACATGGAAGCGCTC 360
 QY 361 CTAGACAGAGACACACAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 CTAGACAGAGACACACAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 AAGTCCGATTCAGAGCTCAGGCGGCTGAGAGTGGTGGAGATCAAGACCGTC 480
 Db 421 AAGTCCGATTCAGAGCTCAGGCGGCTGAGAGTGGTGGAGATCAAGACCGTC 480
 QY 481 AATGCTTACACAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 481 AATGCTTACACAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 541 CCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db 541 CCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 601 AAGATGCTTCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 601 AAGATGCTTCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 661 GCTTTGGGCGAGGCTTCTGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 661 GCTTTGGGCGAGGCTTCTGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 721 AGATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Db 721 AGATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 781 CTCCAGAGAGGCGCGGAGCTTCTTCAACAAAGGTTCAAGGCTTCTTCTGCTGCT 840
 Db 781 CTCCAGAGAGGCGCGGAGCTTCTTCAACAAAGGTTCAAGGCTTCTTCTGCTGCT 840
 QY 841 GCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 841 GCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 901 GCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 901 GCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 GCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 961 GCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

RESULT 9

US-08-284-522B-37
 ; Sequence 37, Application US/08294522B
 ; Patent No. 5741666
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,522B
 FILING DATE: 23-AUG-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..912
 US-08-294-522B-37

Query Match 66.5%; Score 618; DB 1; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6,8e-158;
 Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

QY 1 ATGTTGGGTTCAAGGCCAAGATGTGCCCCCTACTGTCGCACTGTGAAGTTCTTGGGGCT 60
 DB 1 ATGTTGGTTTCAAGGCCAAGATGTGCCCCCAACGCCACTGTGAAGTTCTTGGGGCT 60
 QY 61 GGACAGCTGCTGTCGATGCAAGATCTATCACTTCTCTGTGATCTGCTAAAGTCCG 120
 DB 61 GGACAGCTGCTGTCGATGCAAGATCTATCACTTCTCTGTGATCTGCTAAAGTCCG 120
 QY 121 TTACAGATCCAGAGAAAGTCAGGGGCGAGTGGCGGTACAGCCAGCCAGTACCGG 180
 DB 121 TTACAGATCCAGAGAAAGTCAGGGGCGAGTGGCGGTACAGCCAGCCAGTACCGG 180
 QY 121 CTGCAAGATCCAGAGAAAGTCAGGGGCGAGTGGCGGTACAGCCAGCCAGTACCGG 180
 DB 121 CTGCAAGATCCAGAGAAAGTCAGGGGCGAGTGGCGGTACAGCCAGCCAGTACCGG 180
 QY 181 GGTGTGATGGGCAACCATCTGTAACAATGTGTGCTACTGAGGGCCCCGAGCCTTCAAT 240
 DB 181 GGTGTGATGGGCAACCATCTGTAACAATGTGTGCTACTGAGGGCCCCGAGCCTTCAAT 240
 QY 241 GGGCTGTGTCGGGCTGAGAGCCCAATGAGCTTTGCTTCCGCGATCGGCTGTAT 300
 DB 241 GGGCTGTGTCGGGCTGAGAGCCCAATGAGCTTTGCTTCCGCGATCGGCTGTAT 300
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 DB 241 GGGCTGTGTCGGGCTGAGAGCCCAATGAGCTTTGCTTCCGCGATCGGCTGTAT 300
 QY 301 GATCTGTCAAAAGTTCTTACACCAAGGCTCTGAGCATGCGACATGGAGCGGCTC 360
 DB 301 GATCTGTCAAAAGTTCTTACACCAAGGCTCTGAGCATGCGACATGGAGCGGCTC 360
 QY 301 GATCTGTCAAAAGTTCTTACACCAAGGCTCTGAGCATGCGACATGGAGCGGCTC 360
 DB 301 GATCTGTCAAAAGTTCTTACACCAAGGCTCTGAGCATGCGACATGGAGCGGCTC 360
 QY 361 CTAGCAGCAGACCAACAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 361 CTAGCAGCAGACCAACAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 QY 361 CTAGCAGCAGACCAACAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 361 CTAGCAGCAGACCAACAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 QY 421 AAGGTCCGATTCGAAGCTCAGGCCCGGCTGAGGCTGTGAGATACCAAGACCGCT 480
 DB 421 AAGGTCCGATTCGAAGCTCAGGCCCGGCTGAGGCTGTGAGATACCAAGACCGCT 480
 QY 421 AAGGTCCGATTCGAAGCTCAGGCCCGGCTGAGGCTGTGAGATACCAAGACCGCT 480
 DB 421 AAGGTCCGATTCGAAGCTCAGGCCCGGCTGAGGCTGTGAGATACCAAGACCGCT 480
 QY 481 AATGCTTACAGAACCTTGTCCGAGAGAAAGGTTCCGGGCTCTGTGAAGGAGCTCT 540
 DB 481 AATGCTTACAGAACCTTGTCCGAGAGAAAGGTTCCGGGCTCTGTGAAGGAGCTCT 540
 QY 481 AATGCTTACAGAACCTTGTCCGAGAGAAAGGTTCCGGGCTCTGTGAAGGAGCTCT 540
 DB 481 AATGCTTACAGAACCTTGTCCGAGAGAAAGGTTCCGGGCTCTGTGAAGGAGCTCT 540
 QY 541 CCCAATGTTGCTGTATGCACTTGTCACTGTGTGAGCTGTGAGCTTATGACTATC 600
 DB 541 CCCAATGTTGCTGTATGCACTTGTCACTGTGTGAGCTGTGAGCTTATGACTATC 600
 QY 541 CCCAATGTTGCTGTATGCACTTGTCACTGTGTGAGCTGTGAGCTTATGACTATC 600
 DB 541 CCCAATGTTGCTGTATGCACTTGTCACTGTGTGAGCTGTGAGCTTATGACTATC 600
 QY 601 AAGATGCTCTCTCTGAAGCACTTATGACATGATGATCTCTCTCTCTCTCTCTCT 660
 DB 601 AAGATGCTCTCTCTGAAGCACTTATGACATGATGATCTCTCTCTCTCTCTCTCT 660
 QY 601 AAGATGCTCTCTCTGAAGCACTTATGACATGATGATCTCTCTCTCTCTCTCTCT 660
 DB 601 AAGATGCTCTCTCTGAAGCACTTATGACATGATGATCTCTCTCTCTCTCTCTCT 660
 QY 661 GCCTTTGGGCGAGGCTTGTGACACTGTCTATGCTGCTCCCTGTGAGATGCTGAAG 720

DB 649 GCCTTGGGGGGGGCTTGTGACCAACCGTATGCTCCCTGTGATGTGTGAAGAG 708
 QY 721 AGATACATGATCT 780
 DB 709 AGATACATGATCT 762
 QY 781 CTCAG 840
 DB 763 TGTCTGGAG 822
 QY 841 GGTTCCTGCAAGCTGTGATGTTCCTGACCTTATGAGCAAGCTTAACAGAGCTTAT 900
 DB 823 GATATCTGCAAGCTGTGATGTTCCTGACCTTATGAGCAAGCTTAAAGAGCTTAT 882
 QY 901 GCCTGCACTTCCCGAG 930
 DB 883 GCCTGCACTTCCCGAG 912

RESULT 10
 US-08-807-861A-36
 Sequence 36, Application US/08807861A
 Patent No. 5853975
 GENERAL INFORMATION:
 APPLICANT: Tarragila, Louis A.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 TITLES OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/807,861A
 FILING DATE: 26-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/518,878
 FILING DATE: 23-AUG-1995
 APPLICATION NUMBER: US 08/470,868
 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER: US 08/294,522
 FILING DATE: 23-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-066
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-807-861A-36

Query Match 66.5%; Score 618; DB 2; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6,8e-158;
 Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

QY 1 ATGTTGGGTTCAAGGCCAAGATGTGCCCCCTACTGTCGCACTGTGAAGTTCTTGGGGCT 60

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1 ATGTTGGTTTCAAGGCCACAGATGTGCCCCCAAGCACTGTAAGTTCTGGGGCT 60
61 GGCACAGCTGCTGCATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCG 120
61 GGCACAGCTGCTGCATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCG 120
121 TTACAGATCCAAAGAGAAAGTCAAGGGGCGAGTGCAGCTACAGCAGGCGCCAGTACCG 180
121 CTGCAGATCCAAAGGAGAGTCAAGGGGCGAGTGCAGCTACAGCAGGCGCCAGTACCG 180
181 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 240
181 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 240
241 GGGCTGTGCGGGGCTGAGGCGCAAAATGAGCTTTGCTGTCGCGCATGCGCTGTAT 300
241 GGGCTGTGCGGGGCTGAGGCGCAAAATGAGCTTTGCTGTCGCGCATGCGCTGTAT 300
301 GATTCTGTCAACAGATTCTACCAAGGGGCTGTAGCATGCGCAGCATTTGGAGCGCTTC 360
301 GATTCTGTCAACAGATTCTACCAAGGGGCTGTAGCATGCGCAGCATTTGGAGCGCTTC 360
361 CTGACAGGAGAGCCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 CTGACAGGAGAGCCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
481 AATGCTTACAAGACCTTGCAGGAGAGAGGCTTCCGGGCTCTGGAAGGAGACTCT 540
481 AATGCTTACAAGACCTTGCAGGAGAGAGGCTTCCGGGCTCTGGAAGGAGACTCT 540
541 CCCATGTGCTGCTGATAGCATTTGCACTGTGCTGAGTGTGACTATGACTATC 600
541 CCCATGTGCTGCTGATAGCATTTGCACTGTGCTGAGTGTGACTATGACTATC 600
601 AAGATGCTGCTGCTGTAAGCCAACTCATGACATGACCTCTCTGCACTTCACTTCT 660
601 AAGATGCTGCTGCTGTAAGCCAACTCATGACATGACCTCTCTGCACTTCACTTCT 660
661 GCGTTGGGGGAGGCTTTCGACCACTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
661 GCGTTGGGGGAGGCTTTCGACCACTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
721 AGATACATGA---CTGCTGGGGGAGTACCAAGGGGCTGCTGCTGCTGCTGCTGCTGCT 780
721 AGATACATGA---CTGCTGGGGGAGTACCAAGGGGCTGCTGCTGCTGCTGCTGCTGCT 780
781 CTGCAGATCCAAAGGAGAGTCAAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
781 CTGCAGATCCAAAGGAGAGTCAAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
841 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 900
841 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 900
901 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 960
901 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 960

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RESULT 11
 US-08-470-868A-36
 ; Sequence 36, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TREATMENT OF Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56

```

CORRESPONDENCE ADDRESS:
ADDRESS: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-599
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEO ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-36

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Query Match 66.5%; Score 618; DB 2; Length 1205;
Best Local Similarity 83.5%; Pred. No. 6, Be-158; Indels 18; Gaps 6;
Matches 777; Conservative 0; Mismatches 135;
1 ATGTTGGTTTCAAGGCCACAGATGTGCCCCCAAGCACTGTAAGTTCTGGGGCT 60
1 ATGTTGGTTTCAAGGCCACAGATGTGCCCCCAAGCACTGTAAGTTCTGGGGCT 60
61 GGCACAGCTGCTGCATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCG 120
61 GGCACAGCTGCTGCATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCG 120
121 TTACAGATCCAAAGAGAAAGTCAAGGGGCGAGTGCAGCTACAGCAGGCGCCAGTACCG 180
121 TTACAGATCCAAAGAGAGAAAGTCAAGGGGCGAGTGCAGCTACAGCAGGCGCCAGTACCG 180
181 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 240
181 GGTGTGATGGGCAACATTTCTGACCAATGTGCTGTAAGTGGGCGCCAGTACCAAT 240
241 GGGCTGTGCGGGGCTGAGGCGCAAAATGAGCTTTGCTGTCGCGCATGCGCTGTAT 300
241 GGGCTGTGCGGGGCTGAGGCGCAAAATGAGCTTTGCTGTCGCGCATGCGCTGTAT 300
301 GATTCTGTCAACAGATTCTACCAAGGGGCTGTAGCATGCGCAGCATTTGGAGCGCTTC 360
301 GATTCTGTCAACAGATTCTACCAAGGGGCTGTAGCATGCGCAGCATTTGGAGCGCTTC 360
361 CTGACAGGAGAGCCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 CTGACAGGAGAGCCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
481 AATGCTTACAAGACCTTGCAGGAGAGAGGCTTCCGGGCTCTGGAAGGAGACTCT 540
481 AATGCTTACAAGACCTTGCAGGAGAGAGGCTTCCGGGCTCTGGAAGGAGACTCT 540
541 CCCATGTGCTGCTGATAGCATTTGCACTGTGCTGAGTGTGACTATGACTATC 600
541 CCCATGTGCTGCTGATAGCATTTGCACTGTGCTGAGTGTGACTATGACTATC 600

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Db      533 -CCCAATGTGCGCCCTAATGCAATGTGACGTGAGTGAACCTATGACCTCATC 591
Qy      601 AAGATGCGCCCTCTCTGAAAGCCAACTCATGACAGATGACTCCCTTCCACTTCACTT 660
Db      592 AAAGATCTCTCTCTGA--GCGACCTCATGACAGATGACTCCCTTCCACTTCACTT 648
Qy      661 GCCTTGGGCGAGGCTTCTGACACCTGATGAGCTCCCTTGAAGCGTCAAGAG 720
Db      649 GCCTTGGGCGGAGGCTTCTGACACCTGATGAGCTCCCTTGAAGCGTCAAGAG 708
Qy      721 AGATACATGAACCTGCGCTTGGGCGAGTACAGTACGCTGCGCACTGTGCGCTTACAG 780
Db      709 AGATACATGA--CTCTGCTGGGCGAGTACAGTACGCTGCGCACTGTGCGCTTAC--A 762
Qy      781 CTCGAGAGAGAGGCGCGCGAGGCTTCTACAAAGGTTCAAGCCCTCTCTCGCGCTG 840
Db      763 TGCTCGAGAGAGAGAGCGCGCGCTTCTACCAAGGAGGTTATGCTTCTCTCGCGCTG 822
Qy      841 GGTTCCTGGAACCTGTGATGTGTGTCACCTATGACAGCTGAAAGCGCTTCAAGCT 900
Db      823 GGATCCTGGAACGTGTGATGTGTGTCACCTATGACAGCTTCAAGAGCGCTTAAATGGCT 882
Qy      901 GCGTGCACCTCCCGAGAGAGCTCCCTTCTGA 930
Db      883 GCGTGCACCTCCCGAGAGAGCTTCTTCTGA 912

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RESULT 12

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US-09-210-681-36
Sequence 36, Application US/09210681
Patent No. 6057109

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GENERAL INFORMATION:

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APPLICANT: Iartagila, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
NUMBER OF SEQUENCES: 64
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:

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CLASSIFICATION:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 863-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-210-681-36

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Query Match 66.5%; Score 618; DB 3; Length 1205;
Best Local Similarity 83.5%; Pred. No. 6,8e-158;
Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

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Qy      1 ATGGTTGGTTCAAGGCCACAGATGAGCCCTTACTGACATGTGAATTTCTTGGAGCT 60
Db      1 ATGGTTGGTTCAAGGCCACAGATGTGCCCCCAAGACACATGTGAATTTCTTGGAGCT 60
Qy      61 GGCACAGCTGCTCTGATTCGAGATCTCATACCTTTCTCTGGATCTGTCTAAATCCGG 120
Db      61 GGCACAGCTGCTCTGATTCGAGATCTCATACCTTTCTCTGGATCTGTCTAAATCCGG 120
Qy      121 TTACAGATCCAGAGAAAGTCAAGGGGCGAGTGCAGCTACAGCCAGCGCCAGTACCGC 180
Db      121 CTGAGATCCAGAGAGAGAGTCAAGGGGCGAGTGCAGCTACAGCCAGCGCCAGTACCGT 180
Qy      181 GGTGTGATGGGACCACTTCTGACATGATGTGCTGACTGAGAGGCCCCCAAGCTTCAAT 240
Db      181 GGCCTTCTGGGTACCACTCTTACCATGATGTGCTGACATGAGGTCACAGAGCTTCAAT 240
Qy      241 GGGCTGTTGCGGCGCTGAGAGGCGCAATGAGCTTGTGCTGCGCATGCGCTGTAT 300
Db      241 GGGCTGTTGCGGCGCTGAGAGGCGCAATGAGCTTGTGCTGCGCATTGGCTTAC 300
Qy      301 GATTCGTCAAGAGTTCTTACCAAGAGGCTCTGAGCATGCGAGTATGGAGCCGCTC 360
Db      301 GATTCGTCAAGAGTTCTTACCAAGAGGCTCTGAGCATGAGGATGAGGATGAGGCGGCTC 360
Qy      361 CTACAGAGCAAGCAAGGAGTGCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 420
Db      361 CTGAGAGTACAGCAAGGAGTGCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 420
Qy      421 AAGTCCGATTCAGAGCTCAAGGCGCGGCTGAGAGGTGTGAGAGTATCCAAAGACCGTC 480
Db      421 AAGTCCGCTTCAGAGCTCAAGGCGCGGCTGAGAGGTGTGAGAGTATCC--AGACACCTG 477
Qy      481 AATGCTTCAAGACCAATGCGCGAGAGAGAGAGGTTCCGCGGCTCTGAAAGGAGCTTC 540
Db      478 TCGAGCTTCAAGACCAATGCGCGAGAGAGAGAGGTTCCGCGGCTCTGAAAGGAGCTTC-- 532
Qy      541 CCCAATGTGCTGATATGCACTTGTCAATGTGCTGAGCTGTGTAACCTATGACCTCATC 600
Db      533 -CCCAATGTGCGGCTAATGCACTTGTCAATGTGCTGAGCTGTGTAACCTATGACCTCATC 591
Qy      601 AAGATGCGCCCTCTCTGAAAGCCAACTCATGACAGATGACTCCCTTCCACTTCACTT 660
Db      592 AAAGATCTCTCTCTGA--GCGACCTCATGACAGATGACTCCCTTCCACTTCACTT 648
Qy      661 GCCTTGGGCGAGGCTTCTGACACCTGATGAGCTCCCTTGAAGCGTCAAGAG 720
Db      649 GCCTTGGGCGGAGGCTTCTGACACCTGATGAGCTCCCTTGAAGCGTCAAGAG 708
Qy      721 AGATACATGAACCTGCGCTTGGGCGAGTACAGTACGCTGCGCACTGTGCGCTTACAG 780
Db      709 AGATACATGA--CTCTGCTGGGCGAGTACAGTACGCTGCGCACTGTGCGCTTAC--A 762
Qy      781 CTCGAGAGAGAGGCGCGCGAGGCTTCTACAAAGGTTCAAGCCCTCTCTCGCGCTG 840
Db      763 TGCTCGAGAGAGAGAGCGCGCGCTTCTACCAAGGAGGTTATGCTTCTCTCGCGCTG 822
Qy      841 GGTTCCTGGAACCTGTGATGTGTGTCACCTATGACAGCTGAAAGCGCTTCAAGCT 900
Db      823 GGATCCTGGAACGTGTGATGTGTGTCACCTATGACAGCTTCAAGAGCGCTTAAATGGCT 882
Qy      901 GCGTGCACCTCCCGAGAGAGCTCCCTTCTGA 930
Db      883 GCGTGCACCTCCCGAGAGAGCTTCTTCTGA 912

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RESULT 13

US-08-946-719A-36
Sequence 36, Application US/08946719A

Patent No. 6121017

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
NUMBER OF SEQUENCES: 64
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/234,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9030
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-719A-36

Query Match 66.5%; Score 618; DB 3; Length 1205;
Best Local Similarity 83.5%; Pred. No. 6,8e-158;

Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

QY 1 ATGCTTGGGTTCAAGGCCACACATGTGCCCCCTACTGCGACTGTGAAGTTCTTGGGGCT 60
DB 1 ATGCTTGGGTTCAAGGCCACACATGTGCCCCCAAGCCACTGTGAAGTTCTTGGGGCT 60
QY 61 GGCACAGCTGCGTCAATCGCAGATCTCAATCACTTCTCTGATCTGTAAGTCCGG 120
DB 61 GGCACAGCTGCGTCAATCGCAGATCTCAATCACTTCTCTGATCTGTAAGTCCGG 120
QY 121 TTACAGATCCAAAGAGAAAGTCAAGGGCCAGTGGCGGCTACACAGCCAGCCAGTACCGC 180
DB 121 CTGACATCCAAAGAGAGAGTCAAGGGCTAGTGGCCACAGCCAGCCAGCCAGTACCGT 180
QY 181 GGTGTATGGGACCACTTCTGACATGTGCGTACTGAGAGGCCCGCAAGCCTTACAAAT 240
DB 181 GGGTCTGTGGTACATCTTACATCAATGATGGCCACTGAGGTCACAGCAGCCTTACAAAT 240
QY 241 GGGCTGTGGCCGGCTTGAAGGCCCAATGAGCTTGGCTCTGTCCGATGAGCCTGTAT 300
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DB 241 GGGCTGTGGCCGGCTTGAAGGCCCAATGAGCTTGGCTCTGTCCGATGAGCCTGTATC 300
QY 301 GATTCGTCAAAAGATTTCTACACCAAGGGCTTGAGCATGCCAGATTGGAGCGGCTC 360
DB 301 GATTCGTCAAAAGATTTCTACACCAAGGGCTTGAGCATGCCAGATTGGAGCGGCTC 360
QY 361 CTACAGAGCACACACAGGTGGCTGTGGCTGTGGTGGCCAGCCAGCATGTGGTA 420
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DB 421 AAGTCCGATTCACAGCTCAGCGCCGGCTGAGGTGTGTGAGATACCAAGCAACCGTC 480
QY 481 AATGCTTCAAAAGACCATTCGCCAGAGAGAGAGGTTCCGGGGCTCTGAGAAAGGACTCT 540
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QY 478 TGAGCTTCAAAAGACCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
DB 478 TGAGCTTCAAAAGACCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
QY 541 CCGAATGTGGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 CCGAATGTGGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 591 -CCCAATGTGGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
DB 591 -CCCAATGTGGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
QY 601 AAGATGCGCTTCTGAGAAAGCCAACTTCATGACAGATGACCTCCCTTCCACTTCTCT 660
DB 601 AAGATGCGCTTCTGAGAAAGCCAACTTCATGACAGATGACCTCCCTTCCACTTCTCT 660
QY 592 AAGATGCGCTTCTGAGAAAGCCAACTTCATGACAGATGACCTCCCTTCCACTTCTCT 648
DB 592 AAGATGCGCTTCTGAGAAAGCCAACTTCATGACAGATGACCTCCCTTCCACTTCTCT 648
QY 661 GCGTTTGGGGGAGGCTTCTGACACACATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 GCGTTTGGGGGAGGCTTCTGACACACATGATGATGATGATGATGATGATGATGATGATG 720
QY 649 GCGTTTGGGGGAGGCTTCTGACACACATGATGATGATGATGATGATGATGATGATGATG 708
DB 649 GCGTTTGGGGGAGGCTTCTGACACACATGATGATGATGATGATGATGATGATGATGATG 708
QY 721 AGATACATGAACTGTGCGCTGGGCGAGTACAGTACAGTACAGTACAGTACAGTACAGT 780
DB 721 AGATACATGAACTGTGCGCTGGGCGAGTACAGTACAGTACAGTACAGTACAGTACAGT 780
QY 709 AGATACATGAACTGTGCGCTGGGCGAGTACAGTACAGTACAGTACAGTACAGTACAGT 762
DB 709 AGATACATGAACTGTGCGCTGGGCGAGTACAGTACAGTACAGTACAGTACAGTACAGT 762
QY 781 CTCCAGAAAGAGGGGCGGCGGCTTCTTAAAGGGTATAGGCTTCTTCTGCGCTTG 840
DB 781 CTCCAGAAAGAGGGGCGGCGGCTTCTTAAAGGGTATAGGCTTCTTCTGCGCTTG 840
QY 763 TGCTGGAGAGAGGAGGCGGCGGCTTCTTAAAGGGTATAGGCTTCTTCTGCGCTTG 822
DB 763 TGCTGGAGAGAGGAGGCGGCGGCTTCTTAAAGGGTATAGGCTTCTTCTGCGCTTG 822
QY 841 GATTCCTGGAACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 841 GATTCCTGGAACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 823 GGATCCTGGAACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
DB 823 GGATCCTGGAACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
QY 901 GCGTGCACCTTCCCGAAGGCGCTCCTTCTGA 930
DB 901 GCGTGCACCTTCCCGAAGGCGCTCCTTCTGA 930
QY 883 GCGTGCACCTTCCCGAAGGCGCTCCTTCTGA 912
DB 883 GCGTGCACCTTCCCGAAGGCGCTCCTTCTGA 912

RESULT 14

US-09-547-983-36
Sequence 36, Application US/09547983

Patent No. 6518402

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,983
FILING DATE: 12-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

Query Match	66.5%;	Score 618;	DB 4;	Length 1205;
Best Local Similarity	83.5%;	Pred. No. 6.8e-158;		
Matches 777; Conservative	0;	Mismatches 135;	Indels 18;	Gaps 6

QY	1	ATGCTTGGGTTCAAGGCCACAGATGtgccccctTACCTGcACCTGtGAAGTtCTTg366CT	60
Db	1	ATGCTTGGTTCAAAGGCCACAGATGtgccccccCAACAGcCACTGtGAAGTtCTTcG366CT	60
QY	61	GGCACACCTGcCCtGCANtCCGAGATcTCATcACtTTCCTGtGANAATGtCTAAAGTCCG3	120
Db	61	GGGACACCTGcCTGcCATtTGCAATtCTCAATcTCTTCCTTCCGtATACCGcCMAAGTCCG3	120
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Db	181	GGcCTTCTGGGTACATcCTTAACcATtGtGcCGcATGAGGtTCACGcAGcCTTCAAT	240
QY	241	GGGCTGtGTGcCGGcCTGCAGcCGCCAAATGACtTtTGcCTCTGTCGcATCGcCTGTAT	300
Db	241	GGGCTGtGTGcCGGcCTGCAGcCGCCAGATGACcCTTGcCTCCGtCCGATtTG3cCTTAC	300
QY	301	GATTCTGtCAAAcAGTtCTTACcCAAGAGGcCTGAGcATtGCAGcATtGGGAGcCGcCTC	360
Db	301	GACTGTGtCAAAcAGTtCTTACcCAAGAGGcCTGAGcATtGAGAGcATtGGGAGcCGcCTC	360
QY	361	CTAGAGGcAGcACCAcAGtGcCTTGGcTGTGcCTGTGcCTGTGcCGCCACCGcCAAGtGTGTGA	420
Db	361	CTGcAGAGtTACcACcAGAGtGcCTTGGcCGcGTGTGTGAAGCCACcCTTACAGATGTGTGA	420
QY	421	AAGTcCCATtCCcAGcCTCAGcCGcCGGcCTGAGcGTGTGcGAGATtTACcAAAGcACCGTC	480
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QY	481	AATGcCTTCAAGcACcATtTGcCCCGAGAGAGGtTTCG3GcGcCTTGGAAAGGACCTCT	540
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Db	533	CCCAATGtGcCCGtAAATGcCATtGTTCATcTGtGCTAGcCTGTGACcCTATGACcCTCATC	591
QY	601	AAGATtGcCCtCTGAAAGcCAcCTcTATGACAGATGAcCTCCcCTTGGcCACTTCAcCTCT	660
Db	592	AAAGATcCTTCTCTGA--GcCAcCTtATACAGATGAcCTCCcCTTGGcCACTTCAcCTCT	648

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QY 721 AGATACATGAACTCTGCCCTTGGGCCAGTACAGTAGAGCGTGGCCATCTGTGCCCTTACATG 780

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QY 841 GGTCTCGAGACGTGGTGAATGTTCTCACTTAATAGCAGCTGAAGACAGCCCTCAATGCT 900

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RESULT 15
US-09-702-705-1014
Sequence 1014, Application US/09702705

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/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaltanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darriick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1014
/ LENGTH: 512
/ TYPE: DNA
/ ORGANISM: Homo sapien
/
US-09-702-705-1014

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Query Match	54.7%	Score 508.8	DB 4	Length 512
Best Local Similarity	99.6%	Pred. No. 1.8e-128		
Matches 510; Conservative	0	Mismatches 2	Indels 0	Gaps 0

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Qy	459	TCGGAGATCCAAAGCACGCTCAATGCTCTACAAGACCATTTGCCGACGAGAGAAAGGTTCCG	51
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QY      639 CCTCCCTTGSCACTTCACTTCTGCTTTGGGGGAGGCTTCTGCAACCACTGTGATGACCTC 698
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 Job time : 77 secs

Fri Feb 6 16:59:29 2004

us-09-884-814-2.rnpb

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 19:27:49 ; Search time 399 Seconds

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Title: US-09-884-814-2

Perfect score: 930

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Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1641816367 residues

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	930	100.0	930	10	US-09-884-814-2
2	930	100.0	930	15	US-10-265-689-2
3	930	100.0	1105	13	US-09-823-886A-3
4	930	100.0	1612	15	US-10-265-689-13
5	930	100.0	1643	13	US-10-240-965-183
6	930	100.0	1646	12	US-10-159-563-344
7	928.4	99.8	930	10	US-09-884-814-5
8	928.4	99.8	930	10	US-09-884-814-7
9	928.4	99.8	930	13	US-10-197-019-2
10	928.4	99.8	930	14	US-10-001-051B-1
11	880.4	94.7	960	13	US-09-567-856-1
12	762	81.9	1575	10	US-09-917-800A-1679
13	508.8	54.7	512	10	US-09-736-457-1014
14	508.8	54.7	512	10	US-09-902-941-1014
15	508.8	54.7	512	10	US-09-849-626-1014

16	508.8	54.7	512	13	US-10-113-872-1014	Sequence 1014, Ap
17	508.8	54.7	512	15	US-10-017-754-1014	Sequence 1014, Ap
18	474	51.0	1231	9	US-09-808-457-1	Sequence 1, Appl1
19	472.4	50.8	1192	9	US-09-134-134-1	Sequence 1, Appl1
20	472.4	50.8	1192	9	US-09-826-507-1	Sequence 1, Appl1
21	442.2	47.5	1725	12	US-10-062-674-1405	Sequence 1405, Ap
22	411	44.2	1132	9	US-09-808-457-3	Sequence 3, Appl1
23	411	44.2	1132	13	US-09-823-886A-5	Sequence 5, Appl1
24	316.4	34.0	318	10	US-09-136-457-1376	Sequence 1376, Ap
25	316.4	34.0	318	10	US-09-902-941-1376	Sequence 1376, Ap
26	316.4	34.0	318	10	US-09-849-626-1376	Sequence 1376, Ap
27	316.4	34.0	318	15	US-10-113-872-1376	Sequence 1376, Ap
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30	286.8	30.8	290	13	US-10-101-510-323	Sequence 323, App
31	247.2	26.6	764	9	US-09-910-943-628	Sequence 628, App
32	216.8	23.3	1631	15	US-10-265-689-10	Sequence 10, Appl
33	216.8	23.3	7578	15	US-10-265-689-29	Sequence 29, Appl
34	216.4	23.3	9314	13	US-10-197-019-1	Sequence 1, Appl1
35	188	20.2	556	13	US-10-027-632-134303	Sequence 134303, Ap
36	188	20.2	556	13	US-10-027-632-134303	Sequence 134303, Ap
37	188	20.2	556	14	US-10-027-632-134303	Sequence 134303, Ap
38	188	20.2	556	14	US-10-027-632-134303	Sequence 134303, Ap
39	179	19.2	9246	15	US-10-265-689-25	Sequence 25, Appl
40	178.6	19.2	847	9	US-09-734-134-5	Sequence 5, Appl1
41	176	18.9	1592	15	US-10-265-689-12	Sequence 12, Appl
42	166.6	17.9	416	10	US-09-960-352-3287	Sequence 3287, Ap
43	159.4	17.1	717	15	US-10-265-689-11	Sequence 11, Appl
44	153	16.5	921	10	US-09-938-842A-761	Sequence 761, App
45	153	16.5	921	12	US-09-938-842A-761	Sequence 761, App

ALIGNMENTS

RESULT 1
US-09-884-814-2
Sequence 2, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chem. Jin-Long
APPLICANT: Amarel M. Catherine
APPLICANT: Tularek Inc.
TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
FILE REFERENCE: 018781-001110US
CURRENT APPLICATION NUMBER: US/09/884, 814
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 09/124,293
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularek)
US-09-884-814-2
Query Match
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Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGTTGGTTCAGGACCAAGATGTCCTTACTGCACTGGAAGTTCTTGGGCT 60
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Db 61 GGCACAGCTGCTGCATGCAGATCTATCACTTCTCTGATCTGCTAAAGTCCG 120

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; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-265-689-2

Query Match      100.0%; Score 930; DB 15; Length 930;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGGTTCAAGGCGCAGATGAGCCCTTACTGCGACATGTAAGTTCTTGGGAGCT
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QY 481 AATGCTTCAAGACCATTTGCCGAGAGAGGTTTCCGGGGCTTCTGGAAAAGGACCTCT
Db 481 AATGCTTCAAGACCATTTGCCGAGAGAGGTTTCCGGGGCTTCTGGAAAAGGACCTCT
QY 541 CCCAATGTTGCTCGTAATGCAATGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT
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RESULT 2
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; Sequence 2: Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICOHER, DANIEL
; APPLICANT: BOULLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08

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 ; Publication No. US20030150022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Newell, Marsha
 ; APPLICANT: Berry-Lowe, Sandra
 ; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
 ; FILE REFERENCE: C1102/7002
 ; CURRENT APPLICATION NUMBER: US/09/823,886A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 60/193,533
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
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 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-823-886A-3

Query Match 100.0%; Score 930; DB 13; Length 1105;
 Best Local Similarity 100.0%; Pred. No. 1,2e-281;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGGTTCAAGGCCCAAGATGTGCCCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 60
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DB 629 CCGAATGTTGCTGTATATGCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
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 DB 669 AAGATGCGCTCTGAAAGCCCACTCATGACATGATGCTCCCTTGCATTTCACTTCT 748
 QY 661 GCTTTGGGAGAGCTTCTGACACATGATGATGCTCCCTTGCATTTCACTTCTGAGAG 720
 DB 749 GCTTTGGGAGAGCTTCTGACACATGATGATGCTCCCTTGCATTTCACTTCTGAGAG 808
 QY 721 AGATACATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 809 AGATACATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
 QY 781 CTCAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 869 CTCAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 928
 QY 841 GGTTCCTGGAACGTGGTATGTCCTCACTATGAGCAGTGAACGAGCCCTCATGGCT 900
 DB 929 GGTTCCTGGAACGTGGTATGTCCTCACTATGAGCAGTGAACGAGCCCTCATGGCT 988
 QY 901 GCTTCGACTTCCCGAGAGGCTCCCTTCTGA 930
 DB 989 GCTTCGACTTCCCGAGAGGCTCCCTTCTGA 1018

RESULT 4

US-10-265-689-13
 ; Sequence 13, Application US/10265689
 ; Publication No. US2003011975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SURWIT, RICHARD S.
 ; APPLICANT: COLLINS, SHEILA A.
 ; APPLICANT: WARDEN, CRAIG H.
 ; APPLICANT: SELDIN, MICHAEL F.
 ; APPLICANT: RICOUARD, DANIEL
 ; APPLICANT: BOULLAUD, FREDERIC
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
 ; FILE REFERENCE: 1579-376
 ; CURRENT APPLICATION NUMBER: US/10/265,689
 ; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/353,645
 ; PRIOR FILING DATE: 1999-07-15
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864
 ; PRIOR FILING DATE: 1997-04-22
 ; PRIOR APPLICATION NUMBER: 60/034,960
 ; PRIOR FILING DATE: 1997-01-15
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1612
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-265-689-13

Query Match 100.0%; Score 930; DB 15; Length 1612;
 Best Local Similarity 100.0%; Pred. No. 1,3e-281;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGGTTCAAGGCCCAAGATGTGCCCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 60
 DB 345 ATGGTTGGTTCAAGGCCCAAGATGTGCCCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 404
 QY 61 GGCACAGCTGCTCGATGCGAATCTATCACTTCTCTGATGATGCTAAAGTCCGG 120
 DB 405 GGCACAGCTGCTCGATGCGAATCTATCACTTCTCTGATGATGCTAAAGTCCGG 464
 QY 121 TTACAGATCCAAAGAGAAAGTCAAGGAGCCAGTGGCGCTCAAGCCAGCCCAATACCGC 180
 DB 465 TTACAGATCCAAAGAGAAAGTCAAGGAGCCAGTGGCGCTCAAGCCAGCCCAATACCGC 524
 QY 181 GGTGTATGGGACCACTTCTGACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

```

; SEQ ID NO 183
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 093687.6
US-10-240-965-183

Query Match      100.0%; Score 930; DB 13; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1,3e-281;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  ATGGTTGGGTTCAAGGCGACAGATGTCCTTACTGACAGTGTGAATTTCTTGAGGCT 60
373  ATGGTTGGGTTCAAGGCGACAGATGTCCTTACTGACAGTGTGAATTTCTTGAGGCT 432
61  GGACAGAGTCTGTCATGCGAGATCTCATACCTTTCTCTGGATATCTGTAAGTCCGG 120
433  GGACAGAGTCTGTCATGCGAGATCTCATACCTTTCTCTGGATATCTGTAAGTCCGG 492
121  TTACAGATCCAGAGAGAAAGTCAAGGGGCGCAGTGCAGCGCTCAAGCCAGCCAGTACCG 180
493  TTACAGATCCAGAGAGAAAGTCAAGGGGCGCAGTGCAGCGCTCAAGCCAGCCAGTACCG 552
181  GGTGTGATGGGACCAATTTCTGACATGTGTCTACTGAGGCTCCCGAAGCTTCTACAT 240
553  GGTGTGATGGGACCAATTTCTGACATGTGTCTACTGAGGCTCCCGAAGCTTCTACAT 612
241  GGGGTGTTCCGGGCGCTGAGAGGCGCAATGAGCTTTGCTGTCCGATCGGCTGTAT 300
613  GGGGTGTTCCGGGCGCTGAGAGGCGCAATGAGCTTTGCTGTCCGATCGGCTGTAT 672
301  GATTCTGTCAAGAGTTCTACACCAAGGCTCTGAGCATGTCAGATTGGAGCCGCTC 360
673  GATTCTGTCAAGAGTTCTACACCAAGGCTCTGAGCATGTCAGATTGGAGCCGCTC 732
361  CTAGCAGGCGACACACAGGTGCTGAGCTGTGAGCTGTGAGCCAGCCAGAGTGTGTA 420
733  CTAGCAGGCGACACACAGGTGCTGAGCTGTGAGCTGTGAGCCAGCCAGAGTGTGTA 792
421  AAGTCCGATTTCCAGGCTCAAGGCTCGAGGCTGAGAGTGTGAGATACCAAGACGCTC 480
793  AAGTCCGATTTCCAGGCTCAAGGCTCGAGGCTGAGAGTGTGAGATACCAAGACGCTC 852
481  AATGCTTCAAGACATTTGCGCGAGAGAGAGGTTCCGGGGCTCTGAAAGGACCTCT 540
853  AATGCTTCAAGACATTTGCGCGAGAGAGAGGTTCCGGGGCTCTGAAAGGACCTCT 912
541  CCCAATGTCTGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 600
913  CCCAATGTCTGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 972
601  AAGATGCTCTCTGTAAGGCACTTCAATGACATGACCTCTCTGTAAGGCACTTCT 660
973  AAGATGCTCTCTGTAAGGCACTTCAATGACATGACCTCTCTGTAAGGCACTTCT 1032
661  GCTTTGGGAGGAGCTCTGCAACATGTCATGCTCTCTCTGTAAGGAGCTGTCAAGC 720
1033  GCTTTGGGAGGAGCTCTGCAACATGTCATGCTCTCTCTGTAAGGAGCTGTCAAGC 1092
721  AGATPACATGAATCTGTGCTGTGGGCGAGTACAGTACGTGGCCACTGTGTCAGT 780
1093  AGATPACATGAATCTGTGCTGTGGGCGAGTACAGTACGTGGCCACTGTGTCAGT 1152
781  CTCAGAGAGAGAGGAGCCCGAGCTTCTCAAGAGGTTATGAGCTCTCTTCTCGGCTG 840
1153  CTCAGAGAGAGAGGAGCCCGAGCTTCTCAAGAGGTTATGAGCTCTCTTCTCGGCTG 1212
841  GGTTCCTGGAACGTGTGATGTTGCTGCTACTATGACAGTGTGAAGAGCCTCATGGCT 900
1213  GGTTCCTGGAACGTGTGATGTTGCTGCTACTATGACAGTGTGAAGAGCCTCATGGCT 1272

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; RESULT 5
US-10-240-965-183
; Sequence 183, Application US/10240965
; Publication No. US20030165924A1
GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, DOV
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAMN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL Program

```

QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 DB 1273 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 1302

RESULT 6

US-10-159-563-344
 ; Sequence 344, Application US/10159563
 ; Publication No. US2004000915421
 ; GENERAL INFORMATION:
 ; APPLICANT: Khan, Javed
 ; APPLICANT: Ringer, Markus
 ; APPLICANT: Peterson, Carsten
 ; APPLICANT: Melzer, Paul
 ; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
 ; TITLE OF INVENTION: DIAGNOSIS AND FOR TREATING THE THERAPY OF SELECT CANCERS
 ; FILE REFERENCE: 11613.56US11
 ; CURRENT APPLICATION NUMBER: US/10/159,563
 ; PRIOR FILING DATE: 2002-12-09
 ; PRIOR FILING DATE: 2002-04-25
 ; NUMBER OF SEQ ID NOS: 444
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 344
 ; LENGTH: 1646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-159-563-344

Query Match 100.0%; Score 930; DB 12; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 1,3e-281;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGCACAGATGCCCCCTACTGCGACGTGAAGTTCTTGAGGCT 60
 DB 381 ATGGTTGGGTTCAAGGCGCACAGATGCCCCCTACTGCGACGTGAAGTTCTTGAGGCT 440
 QY 61 GGCACAGCTGCTGCATCGCAGATCTCATACCTTTCTCTGATGATCTGCTAAAGTCCGG 120
 DB 441 GGCACAGCTGCTGCATCGCAGATCTCATACCTTTCTCTGATGATCTGCTAAAGTCCGG 500
 QY 121 TTACAGATCCAGAGAAAGTGAAGGCGGCGAGGCGGCTACAGGCGGCGGCGGCTACGCG 180
 DB 501 TTACAGATCCAGAGAAAGTGAAGGCGGCGAGGCGGCTACAGGCGGCGGCGGCTACGCG 560
 QY 181 GGTGTGATGGGACCACTTCTGACCATGTGCTGCTGAGGCGGCGGCGGCTTCTTACAT 240
 DB 561 GGTGTGATGGGACCACTTCTGACCATGTGCTGCTGAGGCGGCGGCGGCTTCTTACAT 620
 QY 241 GGGCTGTGCGGCGGCTGAGGCGGCGGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 621 GGGCTGTGCGGCGGCTGAGGCGGCGGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCT 680
 QY 301 GATTCTGTCAACAGTTCTTACACCAAGGCGCTTGAAGCATGCCAGATTGGAGCGGCTC 360
 DB 681 GATTCTGTCAACAGTTCTTACACCAAGGCGCTTGAAGCATGCCAGATTGGAGCGGCTC 740
 QY 361 CTAGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 420
 DB 741 CTAGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 800
 QY 421 AAGGTCGATTCCAGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 480
 DB 801 AAGGTCGATTCCAGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 860
 QY 481 AATGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 540
 DB 861 AATGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 920
 QY 541 CCCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 921 CCCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980

QY 601 AAGATGCCCTCTCGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 660
 DB 981 AAGATGCCCTCTCGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1040
 QY 661 GCTTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 720
 DB 1041 GCTTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1100
 QY 721 AGATACATGAACTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 780
 DB 1101 AGATACATGAACTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1160
 QY 781 CTCCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 840
 DB 1161 CTCCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1220
 QY 841 GGTTCCTGGAACGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 1221 GGTTCCTGGAACGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1280
 QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 DB 1281 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 1310

RESULT 7

US-09-884-814-5
 ; Sequence 5, Application US/09884814
 ; Patent No. US20020127600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jin-long
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: Human uncoupling Protein 2 (hUCP2): Compositions and
 ; TITLE OF INVENTION: Methods of use
 ; FILE REFERENCE: 018781-001110US
 ; CURRENT APPLICATION NUMBER: US/09/884,814
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(930)
 ; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tarragila et al.
 US-09-884-814-5

Query Match 99.8%; Score 928.4; DB 10; Length 930;

Best Local Similarity 99.9%; Pred. No. 3.6e-281;
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGCACAGATGCCCCCTACTGCGACGTGAAGTTCTTGAGGCT 60
 DB 1 ATGGTTGGGTTCAAGGCGCACAGATGCCCCCTACTGCGACGTGAAGTTCTTGAGGCT 60
 QY 61 GGCACAGCTGCTGCATCGCAGATCTCATACCTTTCTCTGATGATCTGCTAAAGTCCGG 120
 DB 61 GGCACAGCTGCTGCATCGCAGATCTCATACCTTTCTCTGATGATCTGCTAAAGTCCGG 120
 QY 121 TTACAGATCCAGAGAAAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTACGCG 180
 DB 121 TTACAGATCCAGAGAAAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTACGCG 180
 QY 181 GGTGTGATGGGACCACTTCTGACCATGTGCTGCTGAGGCGGCGGCGGCGGCGGCTTCTTACAT 240
 DB 181 GGTGTGATGGGACCACTTCTGACCATGTGCTGCTGAGGCGGCGGCGGCGGCGGCTTCTTACAT 240
 QY 241 GGGCTGTGCGGCGGCTGAGGCGGCGGCGGCGGCGGCGGCTTCTGCTGCTGCTGCTGCTGCT 300

Db 241 GGGCTGGTTGCGCGCCGCGCAAGAGAGTTGGCTCTGTCCGATGGGCTGTAT 300
Qy 301 GATTCTGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Db 301 GATTCTGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Qy 361 CTAGCAGGAGCAGCAGGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 361 CTAGCAGGAGCAGCAGGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy 481 AATGCTCAAGAGCATTGCGCGAGAGAGAGGTTCCGGGCTCTGTGAAAGGAGCTCT 540
Db 481 AATGCTCAAGAGCATTGCGCGAGAGAGAGGTTCCGGGCTCTGTGAAAGGAGCTCT 540
Qy 541 CCGAATGTGTCTGTAAATGCGCATTTGCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 CCGAATGTGTCTGTAAATGCGCATTTGCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 601 AAGATGCGCTCCGGAAGGCAACCTGATGACAGATGACCTCCCTGGCACTTCACTCT 660
Db 601 AAGATGCGCTCCGGAAGGCAACCTGATGACAGATGACCTCCCTGGCACTTCACTCT 660
Qy 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 AGATACATGAATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 721 AGATACATGAATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Qy 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTCTCTTCTCCGCTTG 840
Db 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTCTCTTCTCCGCTTG 840
Qy 841 GGTTCCTGGAACGT 900
Db 841 GGTTCCTGGAACGT 900
Qy 901 GCGTGCATTTCCGAGAGGCTCTCTTCTGA 930
Db 901 GCGTGCATTTCCGAGAGGCTCTCTTCTGA 930

RESULT 8

US-09-884-814-7
Sequence 7, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chem. Jin-Long
APPLICANT: Amaral, M. Catherine
TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 018781-00110US
CURRENT APPLICATION NUMBER: US/09/884,814
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 09/124,293
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.

US-09-884-814-7
Query Match 99.8%; Score 928.4; DB 10; Length 930;
Best Local Similarity 99.9%; Pred. 3.6e-281;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTTGGGTTCAAGGCCAGATGTGCCCCCTTACTGCACTGTGAAAGTTCTTTGGGCT 60
Db 1 ATGTTGGGTTCAAGGCCAGATGTGCCCCCTTACTGCACTGTGAAAGTTCTTTGGGCT 60
Qy 61 GGCACAGCTGCTGATGCGAGATTTCACTTCTGATATGCTGAAAGTCCGG 120
Db 61 GGCACAGCTGCTGATGCGAGATTTCACTTCTGATATGCTGAAAGTCCGG 120
Qy 121 TTACAGATCAAGAGAAAGTCAAGGCGCAAGTGTGCGCTTACAGCCAGCCCAATCCG 180
Db 121 TTACAGATCAAGAGAAAGTCAAGGCGCAAGTGTGCGCTTACAGCCAGCCCAATCCG 180
Qy 181 GGTGTGATGGGACCAATCTGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 181 GGTGTGATGGGACCAATCTGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Qy 241 GGGCTGTTGCGGCTGTGAGGCGCAATGAGCTTTGCTTGTCCGATGCGCTGTAT 300
Db 241 GGGCTGTTGCGGCTGTGAGGCGCAATGAGCTTTGCTTGTCCGATGCGCTGTAT 300
Qy 301 GATTCTGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Db 301 GATTCTGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Qy 361 CTAGCAGGAGCAGCAGGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 361 CTAGCAGGAGCAGCAGGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy 481 AATGCTCAAGAGCATTGCGCGAGAGAGAGGTTCCGGGCTCTGTGAAAGGAGCTCT 540
Db 481 AATGCTCAAGAGCATTGCGCGAGAGAGAGGTTCCGGGCTCTGTGAAAGGAGCTCT 540
Qy 541 CCGAATGTGTCTGTAAATGCGCATTTGCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 CCGAATGTGTCTGTAAATGCGCATTTGCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 601 AAGATGCGCTCCGGAAGGCAACCTGATGACAGATGACCTCCCTGGCACTTCACTCT 660
Db 601 AAGATGCGCTCCGGAAGGCAACCTGATGACAGATGACCTCCCTGGCACTTCACTCT 660
Qy 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 AGATACATGAATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 721 AGATACATGAATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Qy 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTCTCTTCTCCGCTTG 840
Db 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTCTCTTCTCCGCTTG 840
Qy 841 GGTTCCTGGAACGT 900
Db 841 GGTTCCTGGAACGT 900
Qy 901 GCGTGCATTTCCGAGAGGCTCTCTTCTGA 930
Db 901 GCGTGCATTTCCGAGAGGCTCTCTTCTGA 930

RESULT 9

US-10-197-019-2

```

; Sequence 2, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-004205
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-2

Query Match          99.8%; Score 928.4; DB 13; Length 930;
Best Local Similarity 99.9%; Pred. No. 3.6e-281;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGGCT 60
DB 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGGCT 60
QY 61 GGACAGCTGCTGTCATGCGAGATCTATCACTTTCTCTGTGATCTGCTAAAGTCCG 120
DB 61 GGACAGCTGCTGTCATGCGAGATCTATCACTTTCTCTGTGATCTGCTAAAGTCCG 120
QY 121 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
DB 121 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
QY 122 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
DB 122 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
QY 181 GGTGTGATGGGACCATCTCTACATGTGTGCTACTGAGGAGGCGCCGAGACCTCTACAT 240
DB 181 GGTGTGATGGGACCATCTCTACATGTGTGCTACTGAGGAGGCGCCGAGACCTCTACAT 240
QY 241 GGGCTGTGCTGCGGCTGCGAGGCGCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
DB 241 GGGCTGTGCTGCGGCTGCGAGGCGCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
QY 241 GGGCTGTGCTGCGGCTGCGAGGCGCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
DB 241 GGGCTGTGCTGCGGCTGCGAGGCGCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
QY 301 GATTCGTCAACAGATTCTACACCAAGGAGCTCTGAGCATGCGACATTGGGAGCGGCTC 360
DB 301 GATTCGTCAACAGATTCTACACCAAGGAGCTCTGAGCATGCGACATTGGGAGCGGCTC 360
QY 361 CTAGCAGGAGCAGCAGCAGAGTGCCTGCTGTGCTGTGCGCCAGCCCGAGATGTGTA 420
DB 361 CTAGCAGGAGCAGCAGCAGAGTGCCTGCTGTGCTGTGCGCCAGCCCGAGATGTGTA 420
QY 421 AAGGTCGATCCAGATCCAGGCGCGGCTGAGAGTGTGCGAGATACCAAGCAGCTC 480
DB 421 AAGGTCGATCCAGATCCAGGCGCGGCTGAGAGTGTGCGAGATACCAAGCAGCTC 480
QY 481 AATGCTTCAACAGACCATTTGCGGAGAGAGAGGTTCCGAGGCTCTGTGAAAGGAGCCTCT 540
DB 481 AATGCTTCAACAGACCATTTGCGGAGAGAGAGGTTCCGAGGCTCTGTGAAAGGAGCCTCT 540
QY 541 CCCAATGTTGCTGTGAAGCCATTTGCAACTGTGTGAGTGTGAGTGTGAGCTTGAACCTATC 600
DB 541 CCCAATGTTGCTGTGAAGCCATTTGCAACTGTGTGAGTGTGAGTGTGAGCTTGAACCTATC 600
QY 601 AAGGATGCGCTCTGTAAGCCCACTCACTGACAGATGACCTCCCTTGCACTTCACTTCT 660
DB 601 AAGGATGCGCTCTGTAAGCCCACTCACTGACAGATGACCTCCCTTGCACTTCACTTCT 660
QY 661 GCGTTTGGGGGAGGCTTCTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGT 720
DB 661 GCGTTTGGGGGAGGCTTCTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGT 720

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QY 721 AGATCACTGACTCTGCTGCGGCGAGTACAGTGGCTGGGCACTGCTGCTTACCAAT 780
DB 721 AGATCACTGACTCTGCTGCGGCGAGTACAGTGGCTGGGCACTGCTGCTTACCAAT 780
QY 781 CTCGAGAGAGAGGCGCGGAGCTTCTACAAAGGTTGATGCTTCTTCTCGCTTG 840
DB 781 CTCGAGAGAGAGGCGCGGAGCTTCTACAAAGGTTGATGCTTCTTCTCGCTTG 840
QY 841 GGTTCCTGGAACGTGTGATGTGTCACCTATGACACCTGAAACGACCTCATGCT 900
DB 841 GGTTCCTGGAACGTGTGATGTGTCACCTATGACACCTGAAACGACCTCATGCT 900
QY 901 GCGTCACTTCCGAGAGGCTCCCTCTGA 930
DB 901 GCGTCACTTCCGAGAGGCTCCCTCTGA 930

RESULT 10
US-10-001-051B-1
; Sequence 1, Application US/10001051B
; Publication No. US20020172958A1
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Wilella
; APPLICANT: Gonzalez, Wilella
; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Weisloeh, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: AGT Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
; TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
; FILE REFERENCE: 019488-003010US
; CURRENT APPLICATION NUMBER: US/10/001,051B
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
US-10-001-051B-1

Query Match          99.8%; Score 928.4; DB 14; Length 930;
Best Local Similarity 99.9%; Pred. No. 3.6e-281;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGGCT 60
DB 1 ATGGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGGCT 60
QY 61 GGACAGCTGCTGTCATGCGAGATCTATCACTTTCTCTGTGATCTGCTAAAGTCCG 120
DB 61 GGACAGCTGCTGTCATGCGAGATCTATCACTTTCTCTGTGATCTGCTAAAGTCCG 120
QY 121 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
DB 121 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
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DB 121 TTACAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGGGCTACAGCCAGCCGCGACCG 180
QY 181 GGTGTGATGGGACCATCTCTACATGTGTGCTACTGAGGAGGCGCCGAGACCTCTACAT 240
DB 181 GGTGTGATGGGACCATCTCTACATGTGTGCTACTGAGGAGGCGCCGAGACCTCTACAT 240
QY 241 GGGCTGTGCTGCGGCTGCGAGGCGCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
DB 241 GGGCTGTGCTGCGGCTGCGAGGCGCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
QY 301 GATTCGTCAACAGATTCTACACCAAGGAGCTCTGAGCATGCGACATTGGGAGCGGCTC 360

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RESULT 11
US-09-567-856-1
/ Sequence 1, Application US/09567856
/ Publication No. US20030170606A1
/ GENERAL INFORMATION:
/ APPLICANT: Huang, Shu-Gui
/ APPLICANT: Chen, Jin-Long
/ APPLICANT: Tularix Inc.
/ TITLE OF INVENTION: High-Throughput Screening Assays for Modulators of
/ TITLE OF INVENTION: Mitochondrial Membrane Potential
/ FILE REFERENCE: 018781-001610US
/ CURRENT APPLICATION NUMBER: US/09/567,856
/ CURRENT FILING DATE: 2000-05-09
/ PRIOR APPLICATION NUMBER: US 60/33,268
/ PRIOR FILING DATE: 1999-05-10
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn Ver. 2.1

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; OTHER INFORMATION: Description of Artificial Sequence:hybrid human
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; OTHER INFORMATION: uncoupling protein 2 (hUCP2) including leader
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; OTHER INFORMATION: sequence from yeastADP/ATP carrier 2 (AAC2)
US-03-567-856-1

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RESULT 12
US-09-917-800A-1679
; Sequence 1679, Application US/09917800A
; Patent No. US20020119462A1

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; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael

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APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling
 FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US/09/917,800A
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/222,580
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/230,029
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/230,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/232,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/235,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/237,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/238,884
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1679
 LENGTH: 1575
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_019354
 US-09-917-800A-1679

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 Best Local Similarity 88.7%; Pred. No. 7,9e-229;
 Matches 825; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 ATGTTGGGTTCAAGGCCCAAGATGTCCCTTACTGACCTGTGAAGTTCTTGGGGCT 60
 DB 345 ATGTTGGTTCAGAGGCCACGATGTCCCTTCAAGCCACCGTGAAGTTCTTGGGGCT 404
 QY 61 GGCACAGCTGCTCATCGCATCTCATCACTTCTCTGTGATCTGTGAATCTGTAAAGTCCG 120
 DB 405 GGCACAGAGCTGTATGTGACATCTCATCACTTCTCTGTGACACCGCAAGTCCG 464
 QY 121 TTACAGATCCAAAGAAAGTCAAGGGCCAGTGGCCCTACAGCCAGCCCTGTACCCG 180
 DB 465 CTGCAATCCCAAGGAGAGTCAAGGGCTACGGCCAGCCGCAAGCCCTGTACCCG 524
 QY 181 GATGATGGGACCATCTGACCATGTGCTGCTAGAGGAGCCCGCAAGCTCTACAT 240
 DB 525 GGCCTGTGGGACCATCTGACCATGTGCTGCTAGAGGAGCCCGCAAGCTCTACAT 584
 QY 241 GGGCTGTGGCCGCTGCAAGCCCAATGAGCTTTCCTTGTCCGATCGCTGTAT 300
 DB 585 GGGCTGTGGCCGCTGCAAGCCCAATGAGCTTTCCTTGTCCGATCGCTGTAT 644
 QY 301 GATTTGTCAACATCTTCAACCAAGGCTCTGAGATGACGATTTGGAGCCGCTC 360
 DB 645 GATCTGTAAACATCTTCAACCAAGGCTCTGAGATGACGATTTGGAGCCGCTC 704
 QY 361 CTAGCAGGACGACCAAGTCCCTGTGCTGTGCTGTGCGCCAGCCAGATGTGTA 420
 DB 705 CTGCAAGGACGACCAAGTCCCTGTGCTGTGCTGTGCGCCAGCTTACATGTGTA 764
 QY 421 AAGTTCATTTCAAGCTCAAGCCCGGCTGAGTGTGGAATACCAAGACGCTC 480
 DB 765 AAGTTCGCTTCAAGCCCGGCTGAGTGTGGAATACCAAGACGCTC 824
 QY 481 AATGCTTCAAGACCATTTGCCGAGAGAGAGGTTCCGAGGCTCTGTGAAAGGACCTCT 540
 DB 825 GAAGCTTCAAGACCATTTGCAAGAGAGAGGATCCGGGCTCTGTGAAAGGACCTCT 884

QY 541 CCCAATGTTGCTGTATATGCCATTTCACTGTGTGTAGCTGTGACCTATGACCTATC 600
 DB 885 CCCAATGTTGCCGAATATCCATTTCACTGTGTGTGTAGCTGTGACCTATGACCTATC 944
 QY 601 AAGATGCTCTTCTTAAAGCCCACTCAAGTACAGTACCTCCCTGCACTTCACTCT 660
 DB 945 AAGATGCTCTTCTTAAAGCCCACTCAAGTACAGTACCTCCCTGCACTTCACTCT 1004
 QY 661 GCCTTTGGGAGGCTTGTGACCACTGTATGCTTCCCTGTAGACGTGTCAAGCG 720
 DB 1005 GCCTTTGGGAGGCTTGTGACCACTGTATGCTTCCCTGTAGACGTGTCAAGCG 1064
 QY 721 AGATCATGATCTGTGCTTGGCCCAAGTACAGTACCTGCTGCTGCTTACATG 780
 DB 1065 AGATCATGATCTGTGCTTGGCCCAAGTACAGTACCTGCTGCTGCTTACATG 1124
 QY 781 CTCGAGAGAGAGGAGCCCGGAGCTTCTTCAAAAGGTTCAAGCTTCTTCTCGCTTG 840
 DB 1125 CTCGAGAGAGAGGAGCCCGGAGCTTCTTCAAAAGGTTCAAGCTTCTTCTCGCTTG 1184
 QY 841 GATTCTGGAAGCTGTGTATTTCTGCTACCTATGAGCTGAAACGAGCCCTATGCT 900
 DB 1185 GATCTGGAAGCTGTGTATTTCTGCTACCTATGAGCTGAAACGAGCCCTATGCT 1244
 QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 DB 1245 GCCTATGATCCCGAGAGGCACTTTTGA 1274

RESULT 13

US-09-736-457-1014
 Sequence 1014, Application US/09736457
 Patent No. US20020168637A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Lodes, Michael A.
 APPLICANT: Fanger, Gary
 APPLICANT: Vedvick, Tom
 APPLICANT: Carter, Darrick
 APPLICANT: Retter, Marc
 APPLICANT: Mannion, Jane
 APPLICANT: Fan, Liqun
 APPLICANT: Wang, Aijun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121, 478C15
 CURRENT APPLICATION NUMBER: US/09/736,457
 CURRENT FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 1864
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 1014
 LENGTH: 512
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-736-457-1014

Query Match 54.7%; Score 508.8; DB 10; Length 512;
 Best Local Similarity 39.6%; Pred. No. 2e-149;
 Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 219 GGGCCCCGGAAGCTCTTACAAATGGGCTGTGCGGCGCTGCAAGCCCAATGAGCTTTC 278
 DB 1 GGGCCCCGGAAGCTCTTACAAATGGGCTGTGCGGCGCTGCAAGCCCAATGAGCTTTC 60
 QY 279 CTCTGTCCGATCGGCTGTATGATTTCTGTCAAAAGTTCTACCAAGGCTCTGAGCA 338
 DB 61 CTCTGTCCGATCGGCTGTATGATTTCTGTCAAAAGTTCTACCAAGGCTCTGAGCA 120
 QY 339 TGCAGCATTTGGAGCCGCTTCTTACAGGCAAGCAAGAGGAGCCCTGAGCTGTGCT 398
 DB 121 TGCAGCATTTGGAGCCGCTTCTTACAGGCAAGCAAGAGGAGCCCTGAGCTGTGCT 180

QY 399 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAGAGCTCAGGCCGAGGTGG 458
Db 181 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAGAGCTCAGGCCGAGGTGG 240
QY 459 TCGGAATACCAAGACCGTCAATGCCCAAGACCAATGGCCGAGGAAAGGTTCCG 518
Db 241 TCGGAATACCAAGACCGTCAATGCCCAAGACCAATGGCCGAGGAAAGGTTCCG 300
QY 519 GGACCTCTGGAAGAGGACCTCTCCCATGTGTGTATGTCATTCATTCATGCTGA 578
Db 301 GGACCTCTGGAAGAGGACCTCTCCCATGTGTGTATGTCATTCATTCATGCTGA 360
QY 579 GCTGTGACCTATGACCTCAATCAAGATGCCCTCTGGAAGGACCACTCAAGACATGA 638
Db 361 GCGGCGACCTATGACCTCAATCAAGATGCCCTCTGGAAGGACCACTCAAGACATGA 420
QY 639 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGATTCAGCTTC 698
Db 421 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGATTCAGCTTC 480
QY 699 CCTGTAGACGTGTCAAGACGATACATGA 730
Db 481 CCTGTAGACGTGTCAAGACGATACATGA 512

RESULT 14
US-09-902-941-1014
; Sequence 1014, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Maranabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902.941
; CURRENT FILING DATE: 2001-07-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-1014

Query Match 54.7%; Score 508.8; DB 10; Length 512;
Best Local Similarity 99.6%; Pred. No. 2e-149; Indels 2; Gaps 0;
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 219 GGCCCCCGAAGCTCTTACAAATGGGCTGTGTGCGGCTTGCAAGCCCAATGAGCTTTGC 278
Db 1 GGCCCCCGAAGCTCTTACAAATGGGCTGTGTGCGGCTTGCAAGCCCAATGAGCTTTGC 60
QY 279 CTCTGTCCGATGGCCCGTATGATTTCTGCAAAAGTTCTACCAAGGAGGCTTGAGCA 338
Db 61 CTCTGTCCGATGGCCCGTATGATTTCTGCAAAAGTTCTACCAAGGAGGCTTGAGCA 120
QY 339 TGCAGACATTGGAGCGGCTCTTACAGGACAGACCAAGGAGGCTTGAGCTTGT 398
Db 121 TGCAGACATTGGAGCGGCTCTTACAGGACAGACCAAGGAGGCTTGAGCTTGT 180
QY 399 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAGAGCTCAGGCCGAGGTGG 458
Db 181 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAGAGCTCAGGCCGAGGTGG 240

QY 459 TCGGAATACCAAGACCGTCAATGCCCAAGACCAATGGCCGAGGAAAGGTTCCG 518
Db 241 TCGGAATACCAAGACCGTCAATGCCCAAGACCAATGGCCGAGGAAAGGTTCCG 300
QY 519 GGACCTCTGGAAGAGGACCTCTCCCATGTGTGTATGTCATTCATTCATGCTGA 578
Db 301 GGACCTCTGGAAGAGGACCTCTCCCATGTGTGTATGTCATTCATTCATGCTGA 360
QY 579 GCTGTGACCTATGACCTCAATCAAGATGCCCTCTGGAAGGACCACTCAAGACATGA 638
Db 361 GCGGCGACCTATGACCTCAATCAAGATGCCCTCTGGAAGGACCACTCAAGACATGA 420
QY 639 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGATTCAGCTTC 698
Db 421 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGATTCAGCTTC 480
QY 699 CCTGTAGACGTGTCAAGACGATACATGA 730
Db 481 CCTGTAGACGTGTCAAGACGATACATGA 512

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; Sequence 1014, Application US/09849626
; Publication No. US20020197699A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Ajun
; APPLICANT: Wang, Tonglong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849.626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1014
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-626-1014

Query Match 54.7%; Score 508.8; DB 10; Length 512;
Best Local Similarity 99.6%; Pred. No. 2e-149; Indels 2; Gaps 0;
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 219 GGCCCCCGAAGCTCTTACAAATGGGCTGTGTGCGGCTTGCAAGGCCCAATGAGCTTTGC 278
Db 1 GGCCCCCGAAGCTCTTACAAATGGGCTGTGTGCGGCTTGCAAGGCCCAATGAGCTTTGC 60
QY 279 CTCTGTCCGATGGCCCGTATGATTTCTGCAAAAGTTCTACCAAGGAGGCTTGAGCA 338
Db 61 CTCTGTCCGATGGCCCGTATGATTTCTGCAAAAGTTCTACCAAGGAGGCTTGAGCA 120
QY 339 TGCAGACATTGGAGCGGCTCTTACAGGACAGACCAAGGAGGCTTGAGCTTGT 398
Db 121 TGCAGACATTGGAGCGGCTCTTACAGGACAGACCAAGGAGGCTTGAGCTTGT 180
QY 399 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAGAGCTCAGGCCGAGGTGG 458
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QY 459 TCGGAATACCAAGACCGTCAATGCCCAAGACCAATGGCCGAGGAAAGGTTCCG 518
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QY 519 GGACCTCTGGAAGAGGACCTCTCCCATGTGTGTATGTCATTCATTCATGCTGA 578

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Db	361	GCCGGCACTATGACCTCATCAAGATGCGCTCTCTGAAAGCCAACTCATGACAGATGA	420
Qy	639	CCTGCTTGGCACTTCACTTGTGCTTGGGGCAAGGCTTCTGCACCACTGTCTATGGCTTC	698
Db	421	CCTGCTTGGCACTTCACTTGTGCTTGGGGCAAGGCTTCTGCACCACTGTCTATGGCTTC	480
Qy	699	CCCTGTAGCGGTGCAAGACGATACATGA	730
Db	481	CCCTGTAGCGGTGCAAGACGATACATGA	512

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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102: /cgn2_6/ptodata/1/pna/US6049_COMB.seq.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	930	100.0	930	1	PCT-US99-06317-2
2	930	100.0	930	1	PCT-US99-17246-1
3	930	100.0	930	2	PCT-US99-06317-2
4	930	100.0	930	2	PCT-US99-17246-1

5	930	100.0	930	16	US-09-124-233-1	Sequence 1, Appl
6	930	100.0	930	20	US-09-153-645-2	Sequence 2, Appl
7	930	100.0	930	37	US-09-884-814-2	Sequence 2, Appl
8	930	100.0	930	49	US-10-265-689-2	Sequence 2, Appl
9	930	100.0	960	1	PCT-US03-00253-131	Sequence 131, App
10	930	100.0	960	1	PCT-US03-00253-131	Sequence 131, App
11	930	100.0	960	50	US-10-336-472-131	Sequence 131, App
12	930	100.0	1105	18	US-09-277-575-7	Sequence 131, App
13	930	100.0	1105	25	US-09-599-760-3	Sequence 3, Appl
14	930	100.0	1105	31	US-09-711-022-7	Sequence 3, Appl
15	930	100.0	1105	31	US-09-711-022A-7	Sequence 3, Appl
16	930	100.0	1105	34	US-09-823-886A-3	Sequence 3, Appl
17	930	100.0	1131	1	PCT-US99-01198-4	Sequence 4, Appl
18	930	100.0	1131	2	PCT-US99-01198-4	Sequence 4, Appl
19	930	100.0	1131	15	US-09-012-218-4	Sequence 4, Appl
20	930	100.0	1185	40	US-09-949-016-3539	Sequence 5, Appl
21	930	100.0	1612	20	US-09-353-645-13	Sequence 13, Appl
22	930	100.0	1612	49	US-10-265-689-13	Sequence 13, Appl
23	930	100.0	1617	47	US-10-170-235-27184	Sequence 27184, A
24	930	100.0	1643	48	US-10-240-965-183	Sequence 183, App
25	930	100.0	1643	73	US-09-195-106-183	Sequence 183, App
26	930	100.0	1646	47	US-10-159-563-344	Sequence 344, App
27	930	100.0	1646	53	US-10-631-467-426	Sequence 426, App
28	928.4	99.8	930	1	PCT-US99-17246-5	Sequence 5, Appl
29	928.4	99.8	930	1	PCT-US99-17246-7	Sequence 5, Appl
30	928.4	99.8	930	2	PCT-US99-17246-5	Sequence 5, Appl
31	928.4	99.8	930	2	PCT-US99-17246-7	Sequence 5, Appl
32	928.4	99.8	930	16	US-09-124-293-5	Sequence 7, Appl
33	928.4	99.8	930	16	US-09-124-293-7	Sequence 7, Appl
34	928.4	99.8	930	37	US-09-884-814-5	Sequence 7, Appl
35	928.4	99.8	930	37	US-09-884-814-7	Sequence 7, Appl
36	928.4	99.8	930	44	US-10-001-051B-1	Sequence 2, Appl
37	928.4	99.8	930	47	US-10-197-019-2	Sequence 2, Appl
38	928.4	99.8	940	1	PCT-US99-01198-5	Sequence 5, Appl
39	928.4	99.8	940	2	PCT-US99-01198-5	Sequence 5, Appl
40	928.4	99.8	940	15	US-09-012-218-5	Sequence 5, Appl
41	928.4	99.8	1596	13	US-08-807-861-38	Sequence 38, Appl
42	928.4	99.8	1596	14	US-08-946-719-38	Sequence 38, Appl
43	928.4	99.8	1882	1	PCT-US99-12623-3	Sequence 3, Appl
44	928.4	99.8	1882	2	PCT-US99-12623-3	Sequence 3, Appl
45	928.4	99.8	1882	15	US-09-093-662-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
PCT-US99-06317-2
; Sequence 2, Application PC/TUS9906317
; GENERAL INFORMATION:
; APPLICANT: Garvey, W. Timothy
; APPLICANT: Argyropoulos, George
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A RISK TO UCP2 AND UCP3
; TITLE OF INVENTION: GENE VARIANT-RELATED AFFILIATIONS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 1913.0069/P
; CURRENT APPLICATION NUMBER: PCT/US99/06317
; CURRENT FILING DATE: 1999-03-23
; EARLIER FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(930)
; OTHER INFORMATION: Note://corresponds to the mRNA for human UCP2
PCT-US99-06317-2
Query Match          100.0%; Score 930; DB 1; Length 930;

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Best Local Similarity 100.0%; Pred. No. 2.5e-237; Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	ATGGTTGGGTTCAAGGCGCAGATGTCCTCCCTCACTGAGTGAAGTTCTTGGGGCT	60	Db	1	ATGGTTGGGTTCAAGGCGCAGATGTCCTCCCTCACTGAGTGAAGTTCTTGGGGCT	60		
QY	61	GGCAGAGTGCCTGATGAGATCTCATGACCTTCTCTGTGATATCTGTAAGTCCG	120	QY	61	GGCAGAGTGCCTGATGAGATCTCATGACCTTCTCTGTGATATCTGTAAGTCCG	120		
Db	61	GGCAGAGTGCCTGATGAGATCTCATGACCTTCTCTGTGATATCTGTAAGTCCG	120	Db	61	GGCAGAGTGCCTGATGAGATCTCATGACCTTCTCTGTGATATCTGTAAGTCCG	120		
QY	121	TTACAGATCCAGAGAAAGTCAGAGGCGATGCGGCTACAGCCAGCCAGTACCG	180	QY	121	TTACAGATCCAGAGAAAGTCAGAGGCGATGCGGCTACAGCCAGCCAGTACCG	180		
Db	121	TTACAGATCCAGAGAAAGTCAGAGGCGATGCGGCTACAGCCAGCCAGTACCG	180	Db	121	TTACAGATCCAGAGAAAGTCAGAGGCGATGCGGCTACAGCCAGCCAGTACCG	180		
QY	181	GGTGTGATGGGACCATCTGACCATGATGCTGATGAGGGCCCCGAAAGCTTCAAT	240	QY	181	GGTGTGATGGGACCATCTGACCATGATGCTGATGAGGGCCCCGAAAGCTTCAAT	240		
Db	181	GGTGTGATGGGACCATCTGACCATGATGCTGATGAGGGCCCCGAAAGCTTCAAT	240	Db	181	GGTGTGATGGGACCATCTGACCATGATGCTGATGAGGGCCCCGAAAGCTTCAAT	240		
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QY	301	GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGCATGCCAGATTGGAGCCGCTC	360	QY	301	GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGCATGCCAGATTGGAGCCGCTC	360		
Db	301	GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGCATGCCAGATTGGAGCCGCTC	360	Db	301	GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGCATGCCAGATTGGAGCCGCTC	360		
QY	361	CTAGCAGGAGGACGACGAGGTCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	420	QY	361	CTAGCAGGAGGACGACGAGGTCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	420		
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Db	421	AAGGTCGATTCAGAGCTCAGGCGCGGCTGAGAGTGTGAGATACCAAGCACCGTC	480	Db	421	AAGGTCGATTCAGAGCTCAGGCGCGGCTGAGAGTGTGAGATACCAAGCACCGTC	480		
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Db	781	CTCCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840	Db	781	CTCCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840		
QY	841	GGTTCTGTGAGAGT	900	QY	841	GGTTCTGTGAGAGT	900		
Db	841	GGTTCTGTGAGAGT	900	Db	841	GGTTCTGTGAGAGT	900		
QY	901	GCTGTGATCTCCCGAGAGGCTCCCTTGA	930	QY	901	GCTGTGATCTCCCGAGAGGCTCCCTTGA	930		
Db	901	GCTGTGATCTCCCGAGAGGCTCCCTTGA	930	Db	901	GCTGTGATCTCCCGAGAGGCTCCCTTGA	930		

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RESULT 2
PCT-US99-17246-1
; Sequence 1, Application PC/TUS9917246
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long

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; APPLICANT: Amaral, M. Catherine
; APPLICANT: Tularek Inc.
; TITLE OF INVENTION: Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-001100PC
; CURRENT APPLICATION NUMBER: PCT/US99/17246
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: US 09/124,293
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(930)
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularek)
PCT-US99-17246-1

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Query Match      100.0%; Score 930; DB 1; Length 930;
Best Local Similarity 100.0%; Pred. No. 2.5e-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 AATGCTTCAAGAACCATTTGCCGAGAGAGAGGTTTCCGGGCTCTGTGAAGGAGACCTCT 540
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DB 541 CCCAATGTGCTCGTAAGCATTTGTCACTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 600
QY 541 CCCAATGTGCTCGTAAGCATTTGTCACTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 600
DB 541 CCCAATGTGCTCGTAAGCATTTGTCACTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 600
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DB 601 AAGGATGCTCTCTGTAAGCACTCATGACAGATGACCTCCCTTGTGCACTTCACTTCT 660
QY 601 AAGGATGCTCTCTGTAAGCACTCATGACAGATGACCTCCCTTGTGCACTTCACTTCT 660
DB 601 AAGGATGCTCTCTGTAAGCACTCATGACAGATGACCTCCCTTGTGCACTTCACTTCT 660
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QY 721 AGATACATGAACCTTGCCTTGGGCGAGTACAGTACGCTGCGCACTGTGCTTACCATG 780
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DB 781 CTCACAGAGAGAGGCGCCCGAGCCTTCTTCAAAAGGTTCTATGCTCTCTTCTCGCTTG 840
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DB 781 CTCACAGAGAGAGGCGCCCGAGCCTTCTTCAAAAGGTTCTATGCTCTCTTCTCGCTTG 840
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DB 841 GGTTCCTGAAACGTGTGATGTTGTGTACCTATGAGCACTGAAACGAGCCCTCATGCT 900
QY 841 GGTTCCTGAAACGTGTGATGTTGTGTACCTATGAGCACTGAAACGAGCCCTCATGCT 900
DB 841 GGTTCCTGAAACGTGTGATGTTGTGTACCTATGAGCACTGAAACGAGCCCTCATGCT 900
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RESULT 3

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PCT-US99-06317-2
Sequence 2, Application PC/TUS9906317

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; GENERAL INFORMATION:
; APPLICANT: Garvey, W. Timothy
; APPLICANT: Argyropoulos, George
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A RISK TO UCP2 AND UCP3
; TITLE OF INVENTION: GENE VARIANT-RELATED AFFILIATIONS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 19113.0069/P
; CURRENT APPLICATION NUMBER: PCT/US99/06317
; CURRENT FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: 60/078,972
; EARLIER FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(930)
; OTHER INFORMATION: Note:/corresponds to the mRNA for human UCP2
PCT-US99-06317-2

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Query Match      100.0%; Score 930; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 2.5e-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTTGGGTTCAAGGCGCAGATGTCCTCCCTACCTGCGCACTGTGAAGTTCTTGGGGCT 60
QY 61 GGCAAGCTGCTGCTGATCGAGATCTCATACCTTTCTCTGTGAATCTGTAAAGTCCG 120
DB 61 GGCAAGCTGCTGCTGATCGAGATCTCATACCTTTCTCTGTGAATCTGTAAAGTCCG 120
QY 61 GGCAAGCTGCTGCTGATCGAGATCTCATACCTTTCTCTGTGAATCTGTAAAGTCCG 120
DB 61 GGCAAGCTGCTGCTGATCGAGATCTCATACCTTTCTCTGTGAATCTGTAAAGTCCG 120
QY 121 TTACAGATCCAGAGAAAGTCAAGGGGCTGAGGGCTCAAGCCAGCCGCAATGCCG 180
DB 121 TTACAGATCCAGAGAAAGTCAAGGGGCTGAGGGCTCAAGCCAGCCGCAATGCCG 180
QY 121 TTACAGATCCAGAGAAAGTCAAGGGGCTGAGGGCTCAAGCCAGCCGCAATGCCG 180
DB 121 TTACAGATCCAGAGAAAGTCAAGGGGCTGAGGGCTCAAGCCAGCCGCAATGCCG 180
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QY 181 GGTGTGATGGGCGACCATCTTGTACCATGATGATGAGGGGCTGAGGGGCTGAGGGGCT 240
DB 181 GGTGTGATGGGCGACCATCTTGTACCATGATGATGAGGGGCTGAGGGGCTGAGGGGCT 240
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DB 241 GGGGTGTTGCGCGGCTGCGAGCGCCAAATGAGCTTTCCTCTGTGCGCATCGGCTGTAT 300
QY 241 GGGGTGTTGCGCGGCTGCGAGCGCCAAATGAGCTTTCCTCTGTGCGCATCGGCTGTAT 300
DB 241 GGGGTGTTGCGCGGCTGCGAGCGCCAAATGAGCTTTCCTCTGTGCGCATCGGCTGTAT 300
QY 301 GATTCTGTCAAAAGTTCTTACCAAGAGGCTGTGAGATGCGAGCATTTGGAGAGCCGCTC 360
DB 301 GATTCTGTCAAAAGTTCTTACCAAGAGGCTGTGAGATGCGAGCATTTGGAGAGCCGCTC 360
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QY 361 CTAGCAGGCGACACCAAGGTGCTGCTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CTAGCAGGCGACACCAAGGTGCTGCTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 420

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D	b		361	CTAGCAGGACGCCAACAGGTGCCTCGGTGGTGGTGTTGGCCACGCCCAAGATGTGTGA	420
Q	y		421	AAGGTCGCAATTCCAAAGCTTAAGGCCCCGGGCTGAGAGTGGTCCGAATAATCAAAGCACCGTC	480
D	b		421	AAGGTCGCAATTCCAAAGCTTAAGGCCCCGGGCTGAGAGTGGTCCGAATAATCAAAGCACCGTC	480
Q	y		481	AATGCTTACAAGACCATTTGCCCCAGAGGAGGGATTCGCGAGGACTCTGTGGAAAAGGAGCCTCT	540
D	b		481	AATGCTTACAAGACCATTTGCCCCAGAGGAGGGATTCGCGAGGACTCTGTGGAAAAGGAGCCTCT	540
Q	y		541	CCCAATGTGTGCTGTAAATGSCAATGTGCAACTGTGTGCTGAGCTGTGACCTATGACTTCATC	600
D	b		541	CCCAATGTGTGCTGTAAATGSCAATGTGCAACTGTGTGCTGAGCTGTGACCTATGACTTCATC	600
Q	y		601	AAGAAGGCCCTCCTTGAAAGCCAAACCCTGACAGATGAGACCTCCCTGGCACTTACCTCT	660
D	b		601	AAGAAGGCCCTCCTTGAAAGCCAAACCCTGACAGATGAGACCTCCCTGGCACTTACCTCT	660
Q	y		661	GCCTTTGGGGCAGGCTTCTTGACCACTGTCAATGCGCTCCCTGTAGACGTGTGCAAGCG	720
D	b		661	GCCTTTGGGGCAGGCTTCTTGACCACTGTCAATGCGCTCCCTGTAGACGTGTGCAAGCG	720
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D	b		721	AGATACATGAATCTGTGCTGCGGCCCAGTACAGTAGACGCTGGCACTGTGCGCTTACCATG	780
Q	y		781	CTCCAGAGAAGAGGGGGCCCCGAGGCTCTCAACAAGGATTCATGCCCTCTTCTCCGCTTG	840
D	b		781	CTCCAGAGAAGAGGGGGCCCCGAGGCTCTCAACAAGGATTCATGCCCTCTTCTCCGCTTG	840
Q	y		841	GGTTCCTGGAACGTGTGATGTGTGCTACCTATGAGACAGCTGAAGAGCCCTCATAGGCT	900
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Q	y		901	GCCGTGCACTTCCCGAAGAGGCTCCCTCTCTGA	930
D	b		901	GCCGTGCACTTCCCGAAGAGGCTCCCTCTCTGA	930
 RESULT 4 PCT-US99-17246-1 ; Sequence 1, Application PC/TUS9917246 ; GENERAL INFORMATION: ; APPLICANT: Chen, Jin-Iong ; APPLICANT: Amaral, M. Catherine ; APPLICANT: Tularik Inc. ; TITLE OF INVENTION: Uncoupling Protein 2 (hUCP2): Compositions and ; TITLE OR INVENTION: Methods of use ; FILE REFERENCE: 018781-001100PC ; CURRENT APPLICATION NUMBER: PCT/US99/17246 ; CURRENT FILING DATE: 1999-07-29 ; EARLIER APPLICATION NUMBER: US 09/124,293 ; EARLIER FILING DATE: 1998-07-29 ; NUMBER OF SEQ ID NOS: 8 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 930 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(930) ; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik) PCT-US99-17246-1					

```

Query Match      100.0%;   Score 930;   Length 930;
Best Local Similarity 100.0%;   Pred. No. 2,56-237;
Matches 930;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1  ATGGTGGGTTTAAAGCCACAGATGTGCCCCCTATGCACTGTGAAGTTTCTGGAGCT 60
Db      1  ATGGTGGGTTTAAAGCCACAGATGTGCCCCCTATGCACTGTGAAGTTTCTGGAGCT 60

```

QY	61	GCGACAGCTGCTGGATGCGAGATCTGATACACCTTCTGTGGATCTGTAAAGTCGG	120
Dp	61	GCGACAGCTGCTGGATGCGAGATCTGATACACCTTCTGTGGATCTGTAAAGTCGG	120
QY	121	TTACAGATTCAGAGGAAAGTCAAGGGGCGAGTCGCGCTCAAGCCAGCCGACATACCG	180
Dp	121	TTACAGATTCAGAGGAAAGTCAAGGGGCGAGTCGCGCTCAAGCCAGCCGACATACCG	180
QY	181	GCGGTGATGGGACCATTTCTGACCATGGTGTGGTACTAGAGGCCCGGAAGCCTCTACAT	240
Dp	181	GCGGTGATGGGACCATTTCTGACCATGGTGTGGTACTAGAGGCCCGGAAGCCTCTACAT	240
QY	241	GGGCTGGTTGCGGCTTGAGGCGCAATGAGCTTTGCTCTGTGCGCATCGGCTCTGTAT	300
Dp	241	GGGCTGGTTGCGGCTTGAGGCGCAATGAGCTTTGCTCTGTGCGCATCGGCTCTGTAT	300
QY	301	GATTCGTCAACAGTTCTACACCAAGGCTCTAGAGATCCAGCAATTGGAGACCGCTC	360
Dp	301	GATTCGTCAACAGTTCTACACCAAGGCTCTAGAGATCCAGCAATTGGAGACCGCTC	360
QY	361	CTAGCAGGCAACCAAGTGCCTGGCTGTGGCTGTGGCCAGCCAGATGGTGGTGA	420
Dp	361	CTAGCAGGCAACCAAGTGCCTGGCTGTGGCTGTGGCCAGCCAGATGGTGGTGA	420
QY	421	AAGGTCGGAATCCAGCTCAGGCCCGGGCTGGAGGTGATCGGAGATACCAAGCACCGTC	480
Dp	421	AAGGTCGGAATCCAGCTCAGGCCCGGGCTGGAGGTGATCGGAGATACCAAGCACCGTC	480
QY	481	AATGCTTACAAAGCCATTGCCGGAAGGAAAGGTTCCGGGGCCCTGTGAAAGGGAACCTCT	540
Dp	481	AATGCTTACAAAGCCATTGCCGGAAGGAAAGGTTCCGGGGCCCTGTGAAAGGGAACCTCT	540
QY	541	CCCAATGTTGCTGGTAAATGCACTGTGCAACTGTGCTGAGCTGTGACCTTATGACCTCATC	600
Dp	541	CCCAATGTTGCTGGTAAATGCACTGTGCAACTGTGCTGAGCTGTGACCTTATGACCTCATC	600
QY	601	AAGGATGCCCTCTGTAAAGCCAACTCAATGACATGACCTCCCTTGACCACTTCACTCT	660
Dp	601	AAGGATGCCCTCTGTAAAGCCAACTCAATGACATGACCTCCCTTGACCACTTCACTCT	660
QY	661	GCCTTGGGGCAGGCTTCTGCAACACTGTCATCGCTCCCTGTAGACGTGTGCAAGACG	720
Dp	661	GCCTTGGGGCAGGCTTCTGCAACACTGTCATCGCTCCCTGTAGACGTGTGCAAGACG	720
QY	721	AGATACATGAACCTCCCTGGGSCAGTACAGTACGCTGGCCACTGTGCCCTTACCATG	780
Dp	721	AGATACATGAACCTCCCTGGGSCAGTACAGTACGCTGGCCACTGTGCCCTTACCATG	780
QY	781	CTCCAGAGAGAGGGGCGCCGAGCTTTTACAAAGGCTTCAAGCCCTCTTCTCCGCTTG	840
Dp	781	CTCCAGAGAGAGGGGCGCCGAGCTTTTACAAAGGCTTCAAGCCCTCTTCTCCGCTTG	840
QY	841	GGTTCCTGGAACCTGTGTGATGTGTGCTACACTTATGACAGCTGAACGAGCCCTATGGCT	900
Dp	841	GGTTCCTGGAACCTGTGTGATGTGTGCTACACTTATGACAGCTGAACGAGCCCTATGGCT	900
QY	901	GCCTCGACCTTCCGAGAGGCTCCCTTCTGA 930	
Dp	901	GCCTCGACCTTCCGAGAGGCTCCCTTCTGA 930	

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RESULT 5
US-09-124-293-1
/ Sequence 1 Application US/09124293
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Jin-Long
/ APPLICANT: Amaral, M. Catherine
/ APPLICANT: Tularix Inc.
/ TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
/ TITLE OF INVENTION: Methods of Use
/ FILE REFERENCE: 018781-001100
/ CURRENT APPLICATION NUMBER: US/09/124,293
/ CURRENT FILING DATE: 1998-07-29

```


QY 541 CCCAATGTTGCTGTAATGCCATTTGTAACCTGCTGAGCTGTGATGACCTATGACCTATC 600
 Db 541 CCCAATGTTGCTGTAATGCCATTTGTAACCTGCTGAGCTGTGATGACCTATGACCTATC 600
 QY 601 AAGATGCTCCTCTGAAAGCAACCTATGACGATGACCTCCTTGGCACTTCACTTCT 660
 Db 601 AAGATGCTCCTCTGAAAGCAACCTATGACGATGACCTCCTTGGCACTTCACTTCT 660
 QY 661 GCCTTTGGGCGAGGCTTCTGACCACTGTATGCTCTCCCTGTGATGAGCTGTCAAGC 720
 Db 661 GCCTTTGGGCGAGGCTTCTGACCACTGTATGCTCTCCCTGTGATGAGCTGTCAAGC 720
 QY 721 AGATACATGAACCTGTGCTGCGGCAAGTACAGTACAGGCTGCGCACTGTGCTTACATG 780
 Db 721 AGATACATGAACCTGTGCTGCGGCAAGTACAGTACAGGCTGCGCACTGTGCTTACATG 780
 QY 781 CTCGAGAAGAGGCGCCGAGACCTTCTACAAAGGTTGATGCTCTTCTCCGCTTG 840
 Db 781 CTCGAGAAGAGGCGCCGAGACCTTCTACAAAGGTTGATGCTCTTCTCCGCTTG 840
 QY 841 GGTTCCTGGAACGTGTGATGTCTGCACTTACAGTACAGTACAGGCTGTCAAGCT 900
 Db 841 GGTTCCTGGAACGTGTGATGTCTGCACTTACAGTACAGTACAGGCTGTCAAGCT 900
 QY 901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930
 Db 901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930

RESULT 7

US-09-884-814-2
 ; Sequence 2, Application US/09884814
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 018781-00110US
 ; CURRENT APPLICATION NUMBER: US/09/884,814
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 09/124,293
 ; PRIOR FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(930)
 ; OTHER INFORMATION: human uncoupling Protein 2 (hUCP2) Chen (Tularik)
 ; US-09-884-814-2

Query Match 100.0%; Score 930; DB 37; Length 930;
 Best Local Similarity 100.0%; Pred. No. 2.5e-237;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGGGTTCAAGGCCACAGATGTGCCCCCTTACTGCACTGTGAAGTTCTTGGGGCT 60
 Db 1 ATGTTGGGTTCAAGGCCACAGATGTGCCCCCTTACTGCACTGTGAAGTTCTTGGGGCT 60
 QY 61 GGCACAGCTGCTGATGACGATCTCATCACTTCTCTGATAGTCTTAAAGTCCG 120
 Db 61 GGCACAGCTGCTGATGACGATCTCATCACTTCTCTGATAGTCTTAAAGTCCG 120
 QY 121 TTACAGATCCAAAGGAAAGTCAAGGCGCAAGTGGCGGTACAGCCAGCCGCTACCCG 180
 Db 121 TTACAGATCCAAAGGAAAGTCAAGGCGCAAGTGGCGGTACAGCCAGCCGCTACCCG 180
 QY 181 GGTGTGATGGGACCATTTCTGACATGTGTGTAAGAGGCCCCCGAAGCCTTCAAT 240

Db 181 GGTGTGATGGGACCATTTCTGACATGTGTGTAAGAGGCCCCCGAAGCCTTCAAT 240
 QY 241 GGGCTGTGTGCGGCTGAGCGCCCAATAGACTTTTGCTGTGCGCATGCGCTAT 300
 Db 241 GGGCTGTGTGCGGCTGAGCGCCCAATAGACTTTTGCTGTGCGCATGCGCTAT 300
 QY 301 GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGATGCAAGATTTGGAGCGCTC 360
 Db 301 GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGATGCAAGATTTGGAGCGCTC 360
 QY 361 CTAGCAGGACACCAAGGTGCTTGGCTGTGTGCTGTGCGCCAGCCCAAGATGTGTA 420
 Db 361 CTAGCAGGACACCAAGGTGCTTGGCTGTGTGCTGTGCGCCAGCCCAAGATGTGTA 420
 QY 421 AAGGTCCGATTCGAGCTCAGGCGCGGCTGAGAGTGTGCGAGATACCAAGACCGTC 480
 Db 421 AAGGTCCGATTCGAGCTCAGGCGCGGCTGAGAGTGTGCGAGATACCAAGACCGTC 480
 QY 481 AATGCTTACAAACCATTTGCTGAGAGAGAGGTTCCGAGGCTTGTGAAAGGACCTCT 540
 Db 481 AATGCTTACAAACCATTTGCTGAGAGAGAGGTTCCGAGGCTTGTGAAAGGACCTCT 540
 QY 541 CCCAATGTTGCTGTAATGCCATTTGTAACCTGCTGAGCTGTGATGACCTATGACCTATC 600
 Db 541 CCCAATGTTGCTGTAATGCCATTTGTAACCTGCTGAGCTGTGATGACCTATGACCTATC 600
 QY 601 AAGATGCTCCTCTGAAAGCAACCTATGACGATGACCTCCTTGGCACTTCACTTCT 660
 Db 601 AAGATGCTCCTCTGAAAGCAACCTATGACGATGACCTCCTTGGCACTTCACTTCT 660
 QY 661 GCCTTTGGGCGAGGCTTCTGACCACTGTATGCTCTCCCTGTGATGAGCTGTCAAGC 720
 Db 661 GCCTTTGGGCGAGGCTTCTGACCACTGTATGCTCTCCCTGTGATGAGCTGTCAAGC 720
 QY 721 AGATACATGAACCTGTGCTGCGGCAAGTACAGTACAGGCTGCGCACTGTGCTTACATG 780
 Db 721 AGATACATGAACCTGTGCTGCGGCAAGTACAGTACAGGCTGCGCACTGTGCTTACATG 780
 QY 781 CTCGAGAAGAGGCGCCGAGACCTTCTACAAAGGTTGATGCTCTTCTCCGCTTG 840
 Db 781 CTCGAGAAGAGGCGCCGAGACCTTCTACAAAGGTTGATGCTCTTCTCCGCTTG 840
 QY 841 GGTTCCTGGAACGTGTGATGTCTGCACTTACAGTACAGTACAGGCTGTCAAGCT 900
 Db 841 GGTTCCTGGAACGTGTGATGTCTGCACTTACAGTACAGTACAGGCTGTCAAGCT 900
 QY 901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930
 Db 901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930

RESULT 8

US-10-265-669-2
 ; Sequence 2, Application US/10265669
 ; GENERAL INFORMATION:
 ; APPLICANT: SURMIT, RICHARD S.
 ; APPLICANT: COLLINS, SHEILA A.
 ; APPLICANT: WARDEN, CRAIG H.
 ; APPLICANT: SELDIN, MICHAEL F.
 ; APPLICANT: RIGOUTER, DANIEL
 ; APPLICANT: BOUILLAUD, FREDERIC
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
 ; FILE REFERENCE: 1579-376
 ; CURRENT APPLICATION NUMBER: US/10/265,669
 ; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/353,645
 ; PRIOR FILING DATE: 1999-07-15
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864
 ; PRIOR FILING DATE: 1997-04-22
 ; PRIOR APPLICATION NUMBER: 60/034,960
 ; PRIOR FILING DATE: 1997-01-15
 ; NUMBER OF SEQ ID NOS: 47

Db	375	CTATGCAAGSAGACCAACAGTGTCCCTTGCTGTGGCTGTGGCCCAAGCCCAAGATTGTGTGA	434
QY	421	AAGGTCCGATTCGAAAGCTCAGGCCCCGGGCTGGAGTGTGCGAGATACCAAGCACCTTC	480
Db	435	AAGGTCCGATTCGAAAGCTCAGGCCCCGGGCTGGAGTGTGCGAGATACCAAGCACCTTC	494
QY	481	AATGCTTAAGAACAATTGCCCCGAGAGGAGGGTTCCGCGGCGCTCTGAAAGAGGACCTCT	540
Db	495	AATGCTTAAGAACAATTGCCCCGAGAGGAGGGTTCCGCGGCGCTCTGAAAGAGGACCTCT	554
QY	541	CCCAATGTTGCTGTGATAGCCATTGTCAACTGTGTGAGTGTGTAACCTATGACCTTATC	600
Db	555	CCCAATGTTGCTGTGATAGCCATTGTGCAACTGTGTGTAAGTGTGTAACCTATGACCTTATC	614
QY	601	AAAGATAGCCCTCCTGAAAGCCCAACCTCATAGACAGTAGACCTCCCTTGCACTTACATTC	660
Db	615	AAAGATAGCCCTCCTGAAAGCCCAACCTCATAGACAGTAGACCTCCCTTGCACTTACATTC	674
QY	661	GCGTTTGGGGCAGGCTTTCGACAACACTGTCACTCGCTCCCTGTAGACGTGTCAAGACG	720
Db	675	GCGTTTGGGGCAGGCTTTCGACAACACTGTCACTCGCTCCCTGTAGACGTGTCAAGACG	734
QY	721	AGATACATGAACCTGTGCTCGGCGCAGTACAGTAAAGCGTGGCCACTGTGCCCTTACATG	780
Db	735	AGATACATGAACCTGTGCTCGGCGCAGTACAGTAAAGCGTGGCCACTGTGCCCTTACATG	794
QY	781	CTCCAGAAGAGAGGAGCCCGAGCGCTTCACAAAGGGTTCATAGCCCTCCTTTCGCGCTTG	840
Db	795	CTCCAGAAGAGAGGAGCCCGAGCGCTTCACAAAGGGTTCATAGCCCTCCTTTCGCGCTTG	854
QY	841	GGTTCCTGGAACGTGTGATGTTGTCACCTATAGCAAGCTGAAGAGCCCTCATGGCT	900
Db	855	GGTTCCTGGAACGTGTGATGTTGTCACCTATAGCAAGCTGAAGAGCCCTCATGGCT	914
QY	901	GCCTGCACTTCCCGAGAGGCTCCCTTCTGA	930
Db	915	GCCTGCACTTCCCGAGAGGCTCCCTTCTGA	944

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RESULT 10
PCT-US03-00253-131
; Sequence 131, Application PC/US0300253
; GENERAL INFORMATION:
; APPLICANT: CibaGen Corp. et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-533C-061 (CUA 833C WO)
; CURRENT APPLICATION NUMBER: PCT/US03/00253
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 10/336,472
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/092,900
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 10/136,826
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 10/236,417
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/345,092
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/345,219
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/348,804
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/349,182
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/349,733
; PRIOR FILING DATE: 2002-01-17
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: CuroseqList version 0.1
; SEQ ID NO 131

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; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15) .. (941)
;
PCT-US03-00253-131

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Query Match	100.0%;	Score 930;	DB 2;	Length 960;
Best Local Similarity	100.0%;	Pred. No. 2.6e-237;		
Matches 930;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	ATGGTGGGTTCAAGGCCACAGATGTGCCCTTACCTGACATGTGAAGTTCTTGGAGCT	60
Db	15	ATGGTGGGTTCAAGGCCACAGATGTGCCCTTACCTGACATGTGAAGTTCTTGGAGCT	74
OY	61	GGCACAGCTGCTGCATGCGAGATCTCATCACTTTTCTTGGAATCTGTCTAAAGTCGG	120
Db	75	GGCACAGCTGCTGCATGCGAGATCTCATCACTTTTCTTGGAATCTGTCTAAAGTCGG	134
OY	121	TTACAGATCCAGAGGAAAGTCAGGGGCGAGTGGGGCTACAGCCAGCGCCGAGTACCG	180
Db	135	TTACAGATCCAGAGGAAAGTCAGGGGCGAGTGGGGCTACAGCCAGCGCCGAGTACCG	194
OY	181	GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCGGAAAGCTTACAA	240
Db	195	GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCGGAAAGCTTACAA	254
OY	241	GGGCTGTGTTCCGGGCTGACAGGCCAATGAGCTTTGGCTGTCTGTCCGCAATCGGCTGTAT	300
Db	255	GGGCTGTGTTCCGGGCTGACAGGCCAATGAGCTTTGGCTGTCTGTCCGCAATCGGCTGTAT	314
OY	301	GATTCTGTCAACAGTTTCTACACAGAGGCTCTGAGCATCCAGCAATTGGAGACCGCTTC	360
Db	315	GATTCTGTCAACAGTTTCTACACAGAGGCTCTGAGCATCCAGCAATTGGAGACCGCTTC	374
OY	361	CTTGCAGGCGACACCAAGGTGCTGGCTGTGGCTGTGGCTCCAGCCACGATGTGGTA	420
Db	375	CTTGCAGGCGACACCAAGGTGCTGGCTGTGGCTGTGGCTCCAGCCACGATGTGGTA	434
OY	421	AAAGTCCGATCCAAAGCTCAGGCCCGGGCTGAGGTGATCGAGATTCACAAAGCACCGTC	480
Db	435	AAAGTCCGATCCAAAGCTCAGGCCCGGGCTGAGGTGATCGAGATTCACAAAGCACCGTC	494
OY	481	AATGCTCAACAAGCAATTGCTCCGAGAGGAAAGGTTCCGGGGCTCTTGAAAGGGAACCTCT	540
Db	495	AATGCTCAACAAGCAATTGCTCCGAGAGGAAAGGTTCCGGGGCTCTTGAAAGGGAACCTCT	554
OY	541	CCCAATGTTGCTGTAAATGATTCATTTCAACTGTGTGAGCTGTGACCTTATGACCTATC	600
Db	555	CCCAATGTTGCTGTAAATGATTCATTTCAACTGTGTGAGCTGTGACCTTATGACCTATC	614
OY	601	AAGGATGCTCTCTGAAAGCCAACTCATGACAAATGACTCTCTTGCCCACTTCACTTCT	660
Db	615	AAGGATGCTCTCTGAAAGCCAACTCATGACAAATGACTCTCTTGCCCACTTCACTTCT	674
OY	661	GCGTTGGGGGAGGCTTTCGACCACTGTCAATGCGCTGCCCTGTAAGCGTGTCAAGACG	720
Db	675	GCGTTGGGGGAGGCTTTCGACCACTGTCAATGCGCTGCCCTGTAAGCGTGTCAAGACG	734
OY	721	AGATACATGAATCTTGCTCGGCGCAGTACAGTACGCTGCGCCACTGTGCTCTTACCATG	780
Db	735	AGATACATGAATCTTGCTCGGCGCAGTACAGTACGCTGCGCCACTGTGCTCTTACCATG	794
OY	781	CTCCAGAAAGAGGGGCGCCGAGCTTTCTACAAAGGTTCAAGGCCCTCCTTCTTCGCGTTG	840
Db	795	CTCCAGAAAGAGGGGCGCCGAGCTTTCTACAAAGGTTCAAGGCCCTCCTTCTTCGCGTTG	854
OY	841	GGTTCCTGGAACGTGTGATGTTCGTCACTTATGACAGCTGAACGACGCCCTCATGCT	900
Db	855	GGTTCCTGGAACGTGTGATGTTCGTCACTTATGACAGCTGAACGACGCCCTCATGCT	914
OY	901	GCTGCACTTCCGAGAGGCTCCCTTTCTGA	930

Db 915 GCCTGCACCTCCCGAGAGGCTCCCTCTGA 944

RESULT 11
US-10-336-472-131

Sequence 131, Application US/10336472

GENERAL INFORMATION:

APPLICANT: Anderson, David W.
APPLICANT: Ballinger, Robert A.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Chant, John S.
APPLICANT: Berghs, Constance
APPLICANT: Gangoli, Esna A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Furtak, Katarzyna
APPLICANT: Gerlach, Valerie
APPLICANT: Gilbert, Jennifer A.
APPLICANT: Gunther, Erik
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Ji, Weizhen
APPLICANT: Li, Li
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Paturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Mishra, Vishnu
APPLICANT: Pera, Carol E.A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Shmkeis, Richard A.
APPLICANT: Smithson, Glenda
APPLICANT: Spytek, Kimberly A.
APPLICANT: Stone, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Ore, Tatiana
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Tchiernev, Velizar T.
APPLICANT: Verneil, Corine A.M.
APPLICANT: Wolenc, Adam R.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zhong, Mei

TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-535C
CURRENT APPLICATION NUMBER: US/10/336,472
PRIOR FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/005,041
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 10/023,681
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 10/024,212
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 10/080,334
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/092,900
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 10/136,826
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 10/236,417
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/345,092
PRIOR FILING DATE: 2002-01-04
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 230
SOFTWARE: Cuiaseqdist version 0.1
SEQ ID NO 131
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (15) .. (941)
US-10-336-472-131

Query Match 100.0%; Score 930; DB 50; Length 960;
Best Local Similarity 100.0%; Pred. No. 2,66-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCCCAAGATGTCCTTACTGCGCACTGTGAAGTTTCTTGAGGCT 60
DB 15 ATGGTTGGGTTCAAGGCCCAAGATGTCCTTACTGCGCACTGTGAAGTTTCTTGAGGCT 74
QY 61 GGCAAGCTGCTGCACTGCGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 120
DB 75 GGCAAGCTGCTGCACTGCGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 134
QY 121 TTACAGATCCAGAGAGAAAGTCAAGGCGGCTGCGCTGCAAGCCAGCCGACGACCGC 180
DB 135 TTACAGATCCAGAGAGAAAGTCAAGGCGGCTGCGCTGCAAGCCAGCCGACGACCGC 194
QY 181 GGTGTATGGGCAACCACTTGTGACATGATGGGCTGATGAGGCGCCGGAAGCTCTACAT 240
DB 195 GGTGTATGGGCAACCACTTGTGACATGATGGGCTGATGAGGCGCCGGAAGCTCTACAT 254
QY 241 GGGCTGATGCGCGGCTGCGGCGCAATGAGCTTGTGCTGCGGATGCGCTGAT 300
DB 255 GGGCTGATGCGCGGCTGCGGCGCAATGAGCTTGTGCTGCGGATGCGCTGAT 314
QY 301 GATTCTGTCAAAGTTCTTACACCAAGGCTCTGAGCATGCGAGATTGGAGCGGCTC 360
DB 315 GATTCTGTCAAAGTTCTTACACCAAGGCTCTGAGCATGCGAGATTGGAGCGGCTC 374
QY 361 CTAGCAGGCGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 375 CTAGCAGGCGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
QY 421 AAGTCCGATTCGAAGCTGAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 480
DB 435 AAGTCCGATTCGAAGCTGAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 494
QY 481 ATGCCCTACAAAGCAATGCCGAGAGAGAGGTTCCGGGCTCTGAAAAGGACCTCT 540
DB 495 ATGCCCTACAAAGCAATGCCGAGAGAGAGGTTCCGGGCTCTGAAAAGGACCTCT 554
QY 541 CCCAATGTGCTGTAATGCAATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTGTA 600
DB 555 CCCAATGTGCTGTAATGCAATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTGTA 614
QY 601 AAGGATGCTGCTGTAATGCAATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTG 660
DB 615 AAGGATGCTGCTGTAATGCAATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTG 674
QY 661 GCCCTTGGGCGAGGCTTGTGCAACACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 675 GCCCTTGGGCGAGGCTTGTGCAACACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 734
QY 721 AGATACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 735 AGATACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794
QY 781 CTCGAGAGAGAGGCGCCGAGGCTTCTACAAAGGCTTATGCTGCTGCTGCTGCTGCTGCT 840
DB 795 CTCGAGAGAGAGGCGCCGAGGCTTCTACAAAGGCTTATGCTGCTGCTGCTGCTGCTGCT 854
QY 841 GGTTCCTGAGAGCTGTGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

```

Db      855 GGTTCCTGGAACGTGTATGTTCTGACCTATGACAGCTGAACAGCCCTCATGCT 914
QY      901 GCGTCACTCCCGAGAGGCTCCCTTCTGA 930
Db      915 GCGTCACTCCCGAGAGGCTCCCTTCTGA 944

RESULT 12
US-09-277-575-7
; Sequence 7, Application US/09277575
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha K.
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO
; FILE REFERENCE: WO19/7028/HK
; CURRENT APPLICATION NUMBER: US/09/277,575
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: U.S. 60/082,250
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: U.S. 60/094,519
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: U.S. 60/101,580
; EARLIER FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1105
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-277-575-7

```

```

Query Match      100.0%; Score 930; DB 18; Length 1105;
Best Local Similarity 100.0%; Pred. No. 2.7e-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ATGGTGGGTTCAAGGCGACAGATGTCGCCCTTCTGACCTGTGAAGTTCTTGGGCT 60
Db      89 ATGGTGGGTTCAAGGCGACAGATGTCGCCCTTCTGACCTGTGAAGTTCTTGGGCT 148
QY      61 GGCACAGCTGCTGATCGAGATCTTCATCACTTCTCTGTGATCTGTAAATCCGG 120
Db      149 GGCACAGCTGCTGATCGAGATCTTCATCACTTCTCTGTGATCTGTAAATCCGG 208
QY      121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTTACAGCCAGCCAGTACCC 180
Db      209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTTACAGCCAGCCAGTACCC 268
QY      181 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 240
Db      269 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 328
QY      241 GGGCTGTGTCGGGCTGACAGCCGAAATAGCTTGGCTGTGCGGATCGGCTGTAT 300
Db      329 GGGCTGTGTCGGGCTGACAGCCGAAATAGCTTGGCTGTGCGGATCGGCTGTAT 388
QY      301 GATCTGTCAAAAGTTCTACACCAAGGCTCTGACATGCCAGATTGGAGCCGCTC 360
Db      389 GATCTGTCAAAAGTTCTACACCAAGGCTCTGACATGCCAGATTGGAGCCGCTC 448
QY      361 CTAGCAGCAGACCAAGAGTGGCTGTGCTGTGCGGACCCAGGATGTGTAT 420
Db      449 CTAGCAGCAGACCAAGAGTGGCTGTGCTGTGCGGACCCAGGATGTGTAT 508
QY      421 AAGGTCCGATCCAGGCTCAGGCCCCGCTGAGGTGTGAGATACCAAGACCGTTC 480
Db      509 AAGGTCCGATCCAGGCTCAGGCCCCGCTGAGGTGTGAGATACCAAGACCGTTC 568
QY      491 AATGCTTCAAGACCATTTGCCGAGAGAAAGGTTCCGGGGCTTCTGAAAGGACTCT 540
Db      569 AATGCTTCAAGACCATTTGCCGAGAGAAAGGTTCCGGGGCTTCTGAAAGGACTCT 628
QY      541 CCGATGTGCTCGAATGACCATGTCAACTGTGCTGAGCTGTGACTATGACTATC 600

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Db      629 CCGATGTGCTCGAATGACCATGTCAACTGTGCTGAGCTGTGACTATGACTATC 688
QY      601 AAGATGCCCCCTCGAAGCAACCTCATGACAGATGACCTCCCTGACCTCACTTCT 660
Db      669 AAGATGCCCCCTCGAAGCAACCTCATGACAGATGACCTCCCTGACCTCACTTCT 748
QY      661 GCGTTGGGGGAGGCTTCTGACACCTGTATGCGCTCCCTGTGACAGTGTCAAGAG 720
Db      749 GCGTTGGGGGAGGCTTCTGACACCTGTATGCGCTCCCTGTGACAGTGTCAAGAG 808
QY      721 AATATCATGACTCTGCGCTGGGCACTATAGAGCTGGGCACTGTCCTTACATG 780
Db      809 AATATCATGACTCTGCGCTGGGCACTATAGAGCTGGGCACTGTCCTTACATG 868
QY      781 CTCAGAGAGAGGGGCCCCGAGCCTTCTACAAAGGTTTCATGCTCTCTCTTCCGCTTG 840
Db      869 CTCAGAGAGAGGGGCCCCGAGCCTTCTACAAAGGTTTCATGCTCTCTCTTCCGCTTG 928
QY      841 GGTTCCTGGAACGTGTGATGTGTGACCTATAGAGAGCTGAAAGGCTCATGGCT 900
Db      929 GGTTCCTGGAACGTGTGATGTGTGACCTATAGAGAGCTGAAAGGCTCATGGCT 988
QY      901 GCGTCACTCCCGAGAGGCTCCCTTCTGA 930
Db      989 GCGTCACTCCCGAGAGGCTCCCTTCTGA 1018

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RESULT 13
US-09-599-760-3
; Sequence 3, Application US/09599760
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha K.
; TITLE OF INVENTION: Uncoupling and Products for Manipulating
; FILE REFERENCE: 10277/7009
; CURRENT APPLICATION NUMBER: US/09/599,760
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/140,574
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-599-760-3

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Query Match      100.0%; Score 930; DB 25; Length 1105;
Best Local Similarity 100.0%; Pred. No. 2.7e-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ATGGTGGGTTCAAGGCGACAGATGTCGCCCTTCTGACCTGTGAAGTTCTTGGGCT 60
Db      89 ATGGTGGGTTCAAGGCGACAGATGTCGCCCTTCTGACCTGTGAAGTTCTTGGGCT 148
QY      61 GGCACAGCTGCTGATCGAGATCTTCATCACTTCTCTGTGATCTGTAAAGTCCGG 120
Db      149 GGCACAGCTGCTGATCGAGATCTTCATCACTTCTCTGTGATCTGTAAAGTCCGG 208
QY      121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTTACAGCCAGCCAGTACCC 180
Db      209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTTACAGCCAGCCAGTACCC 268
QY      181 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 240
Db      269 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 328
QY      241 GGGCTGTGTCGGGCTGACAGCCGAAATAGCTTGGCTGTGCGGATCGGCTGTAT 300
Db      329 GGGCTGTGTCGGGCTGACAGCCGAAATAGCTTGGCTGTGCGGATCGGCTGTAT 388
QY      301 GATCTGTCAAAAGTTCTACACCAAGGCTCTGACATGCCAGATTGGAGCCGCTC 360

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; PRIOR FILING DATE: 1998-07-29
 ; PRIOR APPLICATION NUMBER: US 60/101,580
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 7
 ; LENGTH: 1105
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-711-022A-7

Query Match 100.0%; Score 930; DB 31; Length 1105;
 Best Local Similarity 100.0%; Pred. No. 2.7e-237;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTGGGTTCAAGCCACAGATGCCCCCTACTGACAGTGAAGTTCTTGAGGCT	60
DB	89	ATGCTGGGTTCAAGCCACAGATGCCCCCTACTGACAGTGAAGTTCTTGAGGCT	148
QY	61	GGCACAGCTGCTGCATGCGAGATCTCATACCTTTCCTGATATCTGTAAGTCGG	120
DB	149	GGCACAGCTGCTGCATGCGAGATCTCATACCTTTCCTGATATCTGTAAGTCGG	208
QY	121	TTACAGATCCAGAGAAAGTCAAGGCGCAGTCCGCTACAGCCAGCCAGTACCGC	180
DB	209	TTACAGATCCAGAGAAAGTCAAGGCGCAGTCCGCTACAGCCAGCCAGTACCGC	268
QY	181	GGTGTATGGGACCAATCTGACCATGTGCGTACTGAGGCGCCCGAAGCCTCTACAT	240
DB	269	GGTGTATGGGACCAATCTGACCATGTGCGTACTGAGGCGCCCGAAGCCTCTACAT	328
QY	241	GGGCTGTGTCGCGGCTGCGAGCCCAATGAGCTTTGCTGTGCGCATGCGCTGTAT	300
DB	329	GGGCTGTGTCGCGGCTGCGAGCCCAATGAGCTTTGCTGTGCGCATGCGCTGTAT	388
QY	301	GATCTGTCAAAAGTTCTACACCAAGGCTGTGACATGCGAGATTGAGAGCCGCTC	360
DB	389	GATCTGTCAAAAGTTCTACACCAAGGCTGTGACATGCGAGATTGAGAGCCGCTC	448
QY	361	CTAGCAGGACGACACAGAGTGCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	420
DB	449	CTAGCAGGACGACACAGAGTGCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	508
QY	421	AAGGTCCGATTCAGAGTCAAGGCGCGGCTGAGAGTGTGAGATACCAAGCACCGTC	480
DB	509	AAGGTCCGATTCAGAGTCAAGGCGCGGCTGAGAGTGTGAGATACCAAGCACCGTC	568
QY	481	AATGCTCAAGACCATGTCGCGAGAGAAAGGTTCCGAGGCTCTTGAAAGGACCTCT	540
DB	569	AATGCTCAAGACCATGTCGCGAGAGAAAGGTTCCGAGGCTCTTGAAAGGACCTCT	628
QY	541	CCCAATGTGCTCGTAAATGCAATGCTGCTGAGTGTGAGTGTGAGCTATGACCTCATC	600
DB	629	CCCAATGTGCTCGTAAATGCAATGCTGCTGAGTGTGAGTGTGAGCTATGACCTCATC	688
QY	601	AAGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTTGCCACTTCACTTCT	660
DB	689	AAGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTTGCCACTTCACTTCT	748
QY	661	GCTTTGGGGGAGGCTTCTGACCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT	720
DB	749	GCTTTGGGGGAGGCTTCTGACCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT	808
QY	721	AGATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	780
DB	809	AGATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	868
QY	781	CTCCAGAGAGAGGCGCCCGAGCTTCTACAAAGGTTTATGCGCTCTTCTCGGCTTG	840
DB	869	CTCCAGAGAGAGGCGCCCGAGCTTCTACAAAGGTTTATGCGCTCTTCTCGGCTTG	928
QY	841	GGTTCCTGGAAGTGTGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	900

DB	929	GATTCTGGAACGTGTGATGTTGTCACCTATGAGACGTGAACGAGCCCTCATGCT	988
QY	901	GCTGCACTTCCGAGAGGCTCCCTTCTGA	930
DB	989	GCTGCACTTCCGAGAGGCTCCCTTCTGA	1018

Search completed: February 4, 2004, 21:15:07
 Job time : 3501 secs

CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 562
LENGTH: 1617
TYPE: DNA
ORGANISM: Homo sapiens
US-60-485-450-562

Query Match 99.7% Score 927.6; DB 8; Length 1617;
Best Local Similarity 99.5%; Pred. No. 7,66-257;
Matches 925; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Db 1 ATGGTTGGGTTCAAGGCGCACAGATGTGCCCCCTACTGSCACTGTGAAGTTCTTGGGCGT 60
351 ATGGTTGGGTTCAAGGCGCACAGATGTGCCCCCTACTGSCACTGTGAAGTTCTTGGGCGT 410
Qy 61 GGCACAGCTGCTGCTGATGCGAGATCTATCACTTTCTCTGATACTGCTAAAGTCCGG 120
Db 411 GGCACAGCTGCTGCTGATGCGAGATCTATCACTTTCTCTGATACTGCTAAAGTCCGG 470
Qy 121 TTACAGATCCAGAGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCGACGCCAGTACCGC 180
Db 471 TTACAGATCCAGAGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCGACGCCAGTACCGC 530
Qy 181 GGTGTGATGGGACCACTTCTGACCATGTGTGCTAAGAGGCGCCCGAGACCTCTACAT 240
Db 531 GGTGTGATGGGACCACTTCTGACCATGTGTGCTAAGAGGCGCCCGAGACCTCTACAT 590
Qy 241 GGGCTGGTTGCGGCGCTGACAGGCGCAATGAGCTTTCCTGCTGCGCATGCGCTGAT 300
Db 591 GGGCTGGTTGCGGCGCTGACAGGCGCAATGAGCTTTCCTGCTGCGCATGCGCTGAT 650
Qy 301 GATTCGTCAAAACAGTTCTTACACCAAGGCGCTCTGAGCATGCGACATTTGGAGCCGCTC 360
Db 651 GATTCGTCAAAACAGTTCTTACACCAAGGCGCTCTGAGCATGCGACATTTGGAGCCGCTC 710
Qy 361 CTAGCAGGACGACACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 711 CTAGCAGGACGACACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Qy 421 AAGTCCGATTCACAGCTCAGGCGCGGCTGAGGTGCTGAGATACCAAGACCGCTC 480
Db 771 AAGTCCGATTCACAGCTCAGGCGCGGCTGAGGTGCTGAGATACCAAGACCGCTC 830
Qy 481 AATGCTTCAAGACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 831 AATGCTTCAAGACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
Qy 541 CCCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 891 CCCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 950
Qy 601 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 951 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010
Qy 661 GCGTTGGGGGAGGCTTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 1011 GCGTTGGGGGAGGCTTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
Qy 721 AATACATGAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1071 AATACATGAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
Qy 781 CTCACAGAGAGAGGCGCCGAGCTTCTTCAAGAGGCTTCAAGGCTTCTTCTGCGCTG 840
Db 1131 CTCACAGAGAGAGGCGCCGAGCTTCTTCAAGAGGCTTCAAGGCTTCTTCTGCGCTG 1190
Qy 841 GGTTCCTGGAACGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 1191 GGTTCCTGGAACGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250

Qy 901 GCCTGCACTCCCGAGAGGCTCCCTTCTGA 930
Db 1251 GCCTGCACTCCCGAGAGGCTCCCTTCTGA 1280

RESULT 4

US-60-507-481-2199
Sequence 2199, Application US/60507481
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
FILE REFERENCE: AM101084
CURRENT APPLICATION NUMBER: US/60/507,481
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 210107
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2199
LENGTH: 930
TYPE: DNA
ORGANISM: Canis familiaris
US-60-507-481-2199

Query Match 88.2% Score 820.4; DB 8; Length 930;
Best Local Similarity 92.2%; Pred. No. 56-226;
Matches 857; Conservative 6; Mismatches 67; Indels 0; Gaps 0;

Qy 1 ATGGTTGGGTTCAAGGCGCACAGATGTGCCCCCTACTGSCACTGTGAAGTTCTTGGGCGT 60
Db 1 ATGGTTGGGTTCAAGGCGCACAGATGTGCCCCCTACTGSCACTGTGAAGTTCTTGGGCGT 60
Qy 61 GGCACAGCTGCTGCTGATGCGAGATCTATCACTTTCTCTGATACTGCTAAAGTCCGG 120
Db 61 GGCACAGCTGCTGCTGATGCGAGATCTATCACTTTCTCTGATACTGCTAAAGTCCGG 120
Qy 121 TTACAGATCCAGAGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCGACGCCAGTACCGC 180
Db 121 TTACAGATCCAGAGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCGACGCCAGTACCGC 180
Qy 181 GGTGTGATGGGACCACTTCTGACCATGTGTGCTAAGAGGCGCCCGAGACCTCTACAT 240
Db 181 GGTGTGATGGGACCACTTCTGACCATGTGTGCTAAGAGGCGCCCGAGACCTCTACAT 240
Qy 241 GGGCTGGTTGCGGCGCTGACAGGCGCAATGAGCTTTCCTGCTGCGCATGCGCTGAT 300
Db 241 GGGCTGGTTGCGGCGCTGACAGGCGCAATGAGCTTTCCTGCTGCGCATGCGCTGAT 300
Qy 301 GATTCGTCAAAACAGTTCTTACACCAAGGCGCTCTGAGCATGCGACATTTGGAGCCGCTC 360
Db 301 GATTCGTCAAAACAGTTCTTACACCAAGGCGCTCTGAGCATGCGACATTTGGAGCCGCTC 360
Qy 361 CTAGCAGGACGACACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 CTAGCAGGACGACACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 421 AAGTCCGATTCACAGCTCAGGCGCGGCTGAGGTGCTGAGATACCAAGACCGCTC 480
Db 421 AAGTCCGATTCACAGCTCAGGCGCGGCTGAGGTGCTGAGATACCAAGACCGCTC 480
Qy 481 AATGCTTCAAGACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 AATGCTTCAAGACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 541 CCCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 CCCAATGTTGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660


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# Remotely Prior Application data removed - See File Wrapper or PAMM
# NUMBER OF SEQ ID NOS: 3518
# SOFTWARE: PatentIn Ver. 2.1
# SEQ ID NO 1024
# LENGTH: 1575
# TYPE: DNA
# ORGANISM: Rattus norvegicus
# FEATURE:
# OTHER INFORMATION: Genbank Accession No. AB010743
US-60-493-007-1024

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Query Match	81.9%	Score 762;	DB 8;	Length 1575;
Best Local Similarity	88.7%;	Pred. No. 4.1e-209;		
Matches 825; Conservative	0;	Mismatches 105;	Indels 0;	Gaps 0;

QY	1	ATGTTGGGTTTCAAGGCCACAGATGTGCCCCCTACTGTGCACATGGAAGTTCTTGAGGCT	60
Db	345	ATGTGTTGGTTTCAAGGCCACCGATGTGCCCCCAACAGCACGCTGAAGTTCTCTGGGGCT	404
QY	61	GGCAGACGTGCTCGATGCGCAGATCTCATCACTTTTCTCTGTGATACTGTCTAAAGTCGG	120
Db	405	GGACACAGACGCTGTATTGTCAGATCTCATCACTTTTCTCTGTAGACACCGCCAAAGTCGG	464
QY	121	TTTCAGATCCAAAGSAAAGATGAGGGGCGAGGGCGCTACAGCACAGCCGACGTACCGC	180
Db	465	CTGAGATCCAAAGSAAAGATGAGGGGCTAGCGGCGACCGCGCCAGCGCCGACGTACCGC	524
QY	181	GGTGTGATGGGCAACCACTTGACCAATGTGTGCTACTGAGGGCCCCGAAAGCTCTACAAAT	240
Db	525	GGCGTGTGGGCAACCACTTCAACCAATGGTGGCACTGAGGGTCCGCGCAAGCTCTACAAAT	584
QY	241	GGGTGTGTTCCGCGCTTGACAGCGCCAAATGAGGCTTTGCTGTGCGCATGTGGGCTGTAT	300
Db	585	GGGTGTGTCCCGGCTTACAGCGCCAAATGAGCTTTGCTGTGCGCATTTGGCTCTAC	644
QY	301	GATCTGTCTAAACAGTTTCTACCAAGGGCTCTGAGCATGCGACATTTGGAGCGGCTTC	360
Db	645	GACTGTCTAAAGCAGTTTCTACCAAGGGCTCAGAGCATGTGAGGCATTTGGAGCGGCTTC	704
QY	361	CTAGCAGGACGACACACAGGTGCTTGGCTGTGGGTGTGGGCGCCACCGAATGTGGTA	420
Db	705	CTGGCAGGTGACACACAGGTGCTTGGGTGTGGGTGTGGGCCAACTTACAGATGTGGTA	764
QY	421	AAGGTCGATTTCCAACTCAGGCGCGGCTGAGGTGTTCGAGATACCAAGACACGCTC	480
Db	765	AAGGTCGCTTTCCAGGCCACAGCGCGGGCTGGCGGTTGCGAAGTACAGAGCATGTC	824
QY	481	AATTCCTTCAAGAACCAATGTGCCGAGAGGAAGGTTTCGGGGCTCTGTGGAAAGGACCTCT	540
Db	825	GAACCTTACAAAGACCAATGTGCACAGAGGAAGGATCCGGGGCTCTGTGGAAAGGACCTCT	884
QY	541	CCCAATGTTCGTGTATGACCATTTGCACTGTGTGAGCTGTGACCTTATGACCTTATC	600
Db	885	CCCAATGTTCGGAATGACCATTTGCACTGTGTGAGCTGTGACCTTATGACCTTATC	944
QY	601	AAGGATCCCTCTCGAAAGCCAACTCATGACATGACCTTCCTCTGCACTTCACTTCT	660
Db	945	AAAGATCTCTCTCGAAAGCCAACTCATGACATGACCTTCCTCTGCACTTCACTTCT	1000
QY	661	GGCTTTGGGGGAGGCTTCTGCAACAATGTCATGCGCTCCCTGTGAGACGTGTCAAGAG	720
Db	1005	GGCTTTGGGGGAGGCTTCTGCAACAACCTGATGTGCTCCCGCTGATGTGTGTAABAAG	106
QY	721	AGATACATGAACTCTGTGCTTGGGCGCAGTACAGTAAAGCTGTGGCACTGTGCTTACATG	780
Db	1065	AGATATATGAACTCTGTGCTTGGGCGCAGTACCAAGGCGGCGCACTGTGCTTACCATG	1120
QY	781	CTCCAGAAAGAGGGGCCCCGAGCTTCTCAAAGGGTTATGCTCTCTTCTGCGCTTG	840
Db	1125	CTCCGAAAGAGGGGCCCCGAACTTCTTACAGGGTTTATGTCTTCTCTTCTGCGCTTG	118
QY	841	GGTTCCTGGAACGTGTGATGTTCTTACCTATGAGCAAGTGAAGAGCCCTTATGGCT	900

D_b 1185 GGATCTGSAACGTAAGTAAITTTGTACTATAAGACACCTCAAAAAGGCCCTGATGCCT 1244
Q_y 901 GCCTGACTTCCCGAGAGCCTCCCTTTCTGA 930
D_b 1245 GCGTATGAATCCCGGAGGACACCTTTTGA 1274

RESULT 7

US-60-531-341-500
; Sequence 500, Application US/60531341

GENERAL INFORMATION:

ADDITIONAL: The General Hospital Corporation doing business as Massachusetts General

APPLICANT: Hospital / Bayer AG

TITLE OF INVENTION: Nucleotide sequences involved in pain

FILE REFERENCE: 17633/2041

CURRENT FILING DATE: 2003-12-19

NUMBER OF SEQ ID NOS: 2587

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SOFTWARE: perl script
CNO ID: NO FOO
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; SEQ ID NO 300
;
; LENGTH: 1575

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TYPE: DNA

ORGANISM: *Rattus norvegicus*
DISTRIBUTION INFORMATION:

PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: Refseq / NM 019354

DATABASE ENTRY DATE: 2003-10-05

US-60-531-341-500

Query Match	81.9%	Score 762	DB 8	Length 1575
Best Local Similarity	88.7%	Pred. No. 4.1e-209		
Matches 825; Conservative	0	Mismatches 105	Indels 0	Gaps 0

QY	1	ATGGTGGGTTCAAGGCCACAGATGTGGCCCTTACCGCACTGTGAAGTTCTTTGGGGCT	60
Db	345	ATGTGTGGTTTCAAGGCCACCGATGTGGCCCCCAACCCGTGAAGTTCTTGGGGGCT	404
QY	61	GGCAGAGCTGCCGTCATCGCAGATCTCATCACTTTTCTCTGATACTCTTAAAGTCGG	120
Db	405	GGGACAGAGCCTCTGTTTGGAGATCTATCATCTTTCCCTTAAACACCGCAAATCCGG	464
QY	121	TTACAGATCCAGAGAAAGTCAAGGGGCACTGCGCCCTACAGCTACGGCCCAATACCGC	180
Db	465	CTCGAGATCCAGAGAGAGTCAAGGGGTACCGGCAACCCCGCACGGCCCAAGTACCGC	524
QY	181	GGGTATATGGGCAACAATTCATCACTGGTGGTACTAGAGGCCCGAAAGCCTTCAAT	240
Db	525	GGGTGTGTGGCAACAATCTTACATGGTGGGCACTAGAGGTCCGGCAGCCTTCAAT	584
QY	241	GGGCTGGTTGCGGCTCGAGCGCCAAATGAGCTTTGCTGTGCGCATCGGCTGTAT	300
Db	585	GGGTGGTGGCGGCTTACAGCGCAGATGAGCTTTGCTGTGCGCATTTGGCTCTTAC	644
QY	301	GATTCTGTCAAAAGTTCTTACACCAAGGGCTCTAGCATCCAGCAATGGAGACGGCCAC	360
Db	645	GACTCTGTAAAGGAGTTTACACCAAGGGCTTCAAGATGAGGCAATGGAGACGGCTTC	704
QY	361	CTAGCAGGCGACACCAAGTGCCTCTGGCTGTGGCTGTGGCCAGCCCAAGATGTGATA	420
Db	705	CTGGCAGGTGACACCAAGTGCCTCTGGCTGTGGCTGTGGCCCAACTTACAGATGTGATA	764
QY	421	AAGTTCGATTCCAAGCTCAGGCCCGGGCTGGAGGTGTGGAGATTCCAAACACCTGTC	480
Db	765	AAGTTCGGTTTCCAGGCCCAAGGCCCGGGCTGGAGGTGTGGAGATTCCAAACACCTGTC	824
QY	481	AATGCCATAAAGCAATGTGCCGAGAGGAAGGTTTCCGGGGCTCTGGAAGGGAACCTCT	540
Db	825	GAACTCTTCAAGACCAATTCACAGAGGAGAGGATTCGGGGCTCTTGGAAGGGAACCTCT	884
QY	541	CCCATATTTCTGTATGCAATTTGCACTGTGTGCTGAGCTGTGACCTTATGACCTTCATC	600
Db	885	CCCATATTTCCGGAATATGCAATTTGCACTGTGAGCTGTGTGACCTTATGACCTTCATC	944
QY	601	AAGGATGCCCTCTGGAAGCAACCTCAATGAGATGACCTCCCTTGCACCTTCACTTCT	660

Db 945 AAGATATCTCTTGAAGCCCACTCATGACAGACACTCCCTTGCACCTTCACTTCT 1004
 QY 661 GCCTTGGGCAAGCTTCTGCAACCACTGATCGCTCCCTGTAAGAGGTGCAAGC 720
 Db 1005 GCCTTGGGCGGGCTTCTGCAACCACTGATCGCTCCCTGTAAGAGGTGCAAGC 1064
 QY 721 AGATACATGAATCTTCTGCGGCGGCACTAGTAGGCGTGGCACTGGCCCTTAACA 780
 Db 1065 AGATATATGAATCTTCTGCGGCGGCACTAGTAGGCGTGGCACTGGCCCTTAACA 1124
 QY 781 CTCAGAGAGAGGGGCGGCGGCACTTCTAACAAGGATTCATGCTCCCTTCTCGCTTG 840
 Db 1125 CTCAGAGAGAGGGGCGGCGGCACTTCTAACAAGGATTCATGCTCCCTTCTCGCTTG 1184
 QY 841 GGTTCCTGGAAGCTGATGATGCTGCACTTATGAGAGCTGAACGAGCTTCACTGCT 900
 Db 1185 GGATCCTGGAAGCTGATGATGCTGCACTTATGAGAGCTGAACGAGCTTCACTGCT 1244
 QY 901 GCCTGACCTTCCGAGAGGCTCCCTTCTGA 930
 Db 1245 GCCTATGATATCCGAGAGGCACTTCTGA 1274

RESULT 8

US-60-507-481-2196
 ; Sequence 2196, Application US/60507481

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounth, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; FILE REFERENCE: AM101084

; CURRENT APPLICATION NUMBER: US/60/507,481

; CURRENT FILING DATE: 2003-10-02

; NUMBER OF SEQ ID NOS: 210107

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2196

; LENGTH: 936

; TYPE: DNA

; ORGANISM: Canis familiaris

US-60-507-481-2196

Query Match 52.9%; Score 492.2; DB 8; Length 936;

Best Local Similarity 72.4%; Pred. No. 2e-133; Indels 12; Gaps 3;

Matches 680; Conservative 2; Mismatches 245; Indels 12; Gaps 3;

QY 1 ATGGTTGGGTTCAAGGCGCAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGCT 60
 Db 1 ATGGTTGGGTTCAAGGCGCAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGCT 60
 QY 61 GGCACAGCTGCTGCAATCGCAGATTCATCACTTTCCTGTAATCTGTAAGTCCGG 120
 Db 61 GGCACAGCTGCTGCAATCGCAGATTCATCACTTTCCTGTAATCTGTAAGTCCGG 120
 QY 61 GGCACAGCTGCTGTTTGTGATCTCTCACTTTCCTGTAATCTGTAAGTCCGG 120
 Db 61 GGCACAGCTGCTGTTTGTGATCTCTCACTTTCCTGTAATCTGTAAGTCCGG 120
 QY 121 TTACAGATCCAGAGAGAAAGTCAAGGCGGCACTGCGGCTTACAGCCGCGCAATACGC 180
 Db 121 CTGCAGATCCAGAGAGAAAGTCAAGGCGGCACTGCGGCTTACAGCCGCGCAATACGC 177
 QY 181 GGTGTGATGGGCACTTCTGCAATGTGCTGTAATGAGGCGGCGGCAAGCTTCAACAT 240
 Db 178 GGTGTGATGGGCACTTCTGCAATGTGCTGTAATGAGGCGGCGGCAAGCTTCAACAT 237
 QY 241 GGGCTGTTGGCGGCTGCAAGCGGCAATGAGTTTGGCTCTGTCCGCAATCGGCTGTAT 300
 Db 238 GGGCTGTTGGCGGCTGCAAGCGGCAATGAGTTTGGCTCTGTCCGCAATCGGCTGTAT 297
 QY 301 GATCTGTCAAAAGCTTCTTACA---CGAAGGCTTGTAGATCCAGCAATGGAGCGCG 357
 Db 298 GATCTGTCAAAAGCTTCTTACA---CGAAGGCTTGTAGATCCAGCAATGGAGCGCG 357
 QY 358 CTCTAGAGGCAACACAGAGTGGCTGCTGTGAGTGTGAGCCAGCCAGGATGTG 417

Db 358 ATTTTGAGAGGCTGACACACAGAGCCATGAGATCATGTGCCAGCCACAGATGTG 417
 QY 418 GTAAAGTCCGATTCACAGC-----TCAGGCGCGGCTGAGAGTGTGGAGATGCCAA 471
 Db 418 GTAAAGTCCGATTCACAGC-----TCAGGCGCGGCTGAGAGTGTGGAGATGCCAA 477
 QY 472 AGCAGCTCAATGCTCTACAGACCATTTGCCGAGAGAGAGAGGTTCCGGGGCTCTGAAA 531
 Db 478 GGGAGATGATGCTCTACAGACCATTTGCCGAGAGAGAGAGGTTCCGGGGCTCTGAAA 537
 QY 532 GGGAGCTTCCCATGTTGCTGCTGTAATGCCATTTGTCACTGTGTGAGCTGTGACTAT 591
 Db 538 GGGAGCTTCCCATGTTGCTGCTGTAATGCCATTTGTCACTGTGTGAGCTGTGACTAT 597
 QY 592 GACCTCATCAAGATGCTCCCTCTGAAGCCCACTCACTGACAGTGAACCTCCCTGCAAC 651
 Db 598 GACATCATCAAGATGCTCCCTCTGAAGCCCACTCACTGACAGTGAACCTCCCTGCAAC 657
 QY 652 TTCACTTGTGCTTGGGCGAGGCTTCTGCAACCTGTCAATGCTTCCCTGTAGAGCTG 711
 Db 658 TTGATTTCTGCTTGGGCGAGGCTTCTGCAACCTGTCAATGCTTCCCTGTAGAGCTG 717
 QY 712 GTCAAGAGAGATATCATGAACTTGCCTGCGGCGGCACTAGTAGGCTGCGCACTGAC 771
 Db 718 GTGAGAGAGAGATATCATGAACTTGCCTGCGGCGGCACTAGTAGGCTGCGCACTGAC 777
 QY 772 CTACCATGCTCCAGAGAGGCGGCGGCGGCGGCTTCTTCAAAAGGTTCAATGCCCTCTT 831
 Db 778 CTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
 QY 832 CTCATGCTGCTGCTGCACTTCCGAGAGGCTTCCCTTCTGA 930
 Db 838 TTGATGAAAGTCCAGATGCTAGCGGAGATTCATCTTCTGA 936

RESULT 9

US-60-490-890-851

; Sequence 851, Application US/60490890

; GENERAL INFORMATION:

; APPLICANT: Li, Martha

; APPLICANT: Rudnow, Brent A.

; APPLICANT: Webster, Kevin R.

; APPLICANT: Jackson, Donald

; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION

; FILE REFERENCE: D0310 PSP

; CURRENT APPLICATION NUMBER: US/60/490,890

; CURRENT FILING DATE: 2003-07-29

; NUMBER OF SEQ ID NOS: 2779

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 851

; LENGTH: 2263

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-490-890-851

Query Match 50.8%; Score 472.4; DB 8; Length 2263;

Best Local Similarity 71.2%; Pred. No. 1.4e-125; Indels 15; Gaps 3;

Matches 671; Conservative 0; Mismatches 256; Indels 15; Gaps 3;

QY 1 ATGGTTGGGTTCAAGGCGCAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGCT 60
 Db 204 ATGGTTGGGTTCAAGGCGCAGATGTGCCCCCTACTGCACTGTGAAGTTTCTTGGGCT 263
 QY 61 GGCACAGCTGCTGCAATCGCAGATTCATCACTTTCCTGTAATCTGTAAGTCCGG 120
 Db 264 GGCACAGCTGCTGTTTGTGATCTCTCACTTTCCTGTAATCTGTAAGTCCGG 323
 QY 121 TTACAGATCCAGAGAGAAAGTCAAGGCGGCACTGCGGCTTACAGCCGCGCAATACGC 180

Dd		324	CTGCAGATTCGAGGGGAGAACAG---CGGTCCAGACGGCCCGGCTGTGTACATACCGT	380
Qy		181	GGTGTGATGGGACCACTTCGACCATGTGTCGATGAGAGGCCCCGAAAGCTTACAT	240
Dd		381	GCGGTGTGGGACCATCTGACCATGTGCGACCTGAGGTTCCCTCGAGCCCCCTACAT	440
Qy		241	GGGCTGTGTTCGCGGCTTCAGCGCCAATGAGCTTTCCTCTGTGCGCATGGGCTGTAT	300
Dd		441	GGGCTGTGTGGCGGCTGCAGACGCACATGATGAGCTTCGCTTCATCGGATCGGCTCTAT	500
Qy		301	GATTCGTGTAAACAGTTCTACA---CCAAAGGCTGTGAGCATTCGACATTTGGAGCCCG	357
Dd		501	GATCTCGTACACAGTGTACACCCCAAGGGCGGAGCAATCCAGCTCTCATACCCGG	560
Qy		358	CTCCTAGCAGCAGCACCAAGTGTGCTGGCTGTGGCTGTGGCCAGCCCAAGATGTG	417
Dd		561	ATTTTGGCCGGCTGCACCAAGAGCCATGGCGGTATCTGTGCCAGCCACAAATGTG	620
Qy		418	GTAAGGTCGATTCGAAGC-----TCAGGCCCGGCTGAGGTGTGTGAGATAC	468
Dd		621	GTAAGGTCCGATTCAGGCCAGGATACACTCGGCGCATTCAGAGCCACAGAAATAC	680
Qy		469	CAAGCAGCCGTGAATGCTTACAAGCACTTGGCCGAGAGGAGGTTCCGGGGCTCTGG	528
Dd		681	AGCGGACTATGGAGCGCTTACAGAACATGCGCAGGAGAGAAAGATCAGGGGCTTGTGG	740
Qy		529	AAAGGACCTTCCCAATGTTGCTGTGATGCCATTGTCAACTGTGCTGAGCTGTGTAC	588
Dd		741	AAAGGAATTTGGCCCAATCATAGGAATCTATCTCAACTGTCTAGGTGTGTAC	800
Qy		589	TATGACCTCATCAAGATGCGCTCTGTAAACCAACTCATGACAAATGACCTCCCTTGC	648
Dd		801	TACGACATCCTCAAGAGAAAGTGTGTGACTATACCTGCTCACTGACAACTTCCCTTGC	860
Qy		649	CACCTCACTTTCGCTTTGGGCGAGCTTTCGACCACTGTCAATGCTTCCCTGTAGAC	708
Dd		861	CACCTTGTCTTTCGCTTTGGAGCGGGCTTCTGTGCAAGTGGTGCCTCCGGTGCAC	920
Qy		709	GTGTGTAAAGACGATACATGAATCTTGTGCTCGGCGCAATGACATGAGCTGGCACATGT	768
Dd		921	GTGTGTAAAGCCGGGTATATGAACCTCACTTCAGGCCAGATCTTCAGCCCCCTGTGACT	980
Qy		769	GCCCTTACATGCTCTCAGAAAGAGGGGCCCCGAGCCTTCTTCAAAAGGTTTATGCCCCCT	828
Dd		981	ATGATTAAGATGTGTGCCCCAGAGGGCCCCCAAGCTTCTTCAAAAGGATTTTACACCTTCC	1040
Qy		829	TTTCTGCGCTTGGGTCTGTGAACGTGTGATGTTGTCACCTATGAGCACTGTAAACGA	888
Dd		1041	TTTTTGGTTTGGGATCTGTGAACGTGTGTGATGTTGTAACTTATGAGCAGCTGAACGG	1100
Qy		889	GGCCTATGCTGCTGCACTTCCGAGAGGATCCCTCTTGA	930
Dd		1101	GCCCTGATGAAGTCCAGATGTTTACGGGATCACCGCTTTTGA	1142

```

RESULT 10
PCT-US03-10141-263
Sequence 263, Application PC/TUS0310141
GENERAL INFORMATION:
APPLICANT: PHASE-1 Molecular Toxicology, Inc.
APPLICANT: Kier, Larry
APPLICANT: Nolan, Timothy D.
APPLICANT: Sankar, Usha
APPLICANT: Darbel, Mober
TITLE OF INVENTION: Liver Necrosis Predictive Genes
FILE REFERENCE: 2874-022PCT
CURRENT APPLICATION NUMBER: PCT/US03/10141
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: US 60/369,287
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FASTSEQ for Windows Version 4.0

```

```

1 SEQ ID NO 263
2
3 LENGTH: 674
4
5 TYPE: DNA
6
7 ORGANISM: Artificial Sequence
8
9 FEATURE:
10
11 OTHER INFORMATION: predictive genes for liver necrosis
12
13 FEATURE:
14
15 NAME/KEY: misc_feature
16
17 LOCATION: 1
18
19 OTHER INFORMATION: n = A,T,C or G
20
21 PCT-US03-10141-263

```

Query Match	45.3%;	Score 421.4;	DB 1;	Length 674;
Best Local Similarity	91.6%;	Pred. No. 4.6e-111;		
Matches 446;	Conservative	0;	Mismatches 41;	Indels 0;
			Gaps	0

QY	368	GCAAGCACCAAGTGGCTGCTGTGTGTGTGTGGCCAGCCACAGAGTGTGTAAAGATCC	427
Db	88	GGAGCAACCAAGATGCTCCCTGGCTGTGGGTGTGGCCCACTTAAGATGTGTAAAGATCC	147
QY	428	GATTCACAACTACAGGCCCGAGCTGAGGTGTGTGGAGATACAAAGCACCGTCATGCTT	487
Db	148	GCTTCCAGGCCACAGGCCCGAGCTGGCGGTGTGTGGAGATACCAAGACATGTGAAGCTT	207
QY	488	ACAAAGCACTTGGCCCCGAGAGAAAGGATTCGGGGGCTCTGAAAGAGGAGCTCTCCCAATG	547
Db	208	ACAAGACACTTGAACGAGAGGAGGATTCGGGGCTCTGAAAGAGGAGCTCTCCCAATG	267
QY	548	TTGCTGTATGTCATTGTCACTGTGTGAGCTGTGAGCTTATGACTTCATCAAGATG	607
Db	268	TTGCCCCGAATGCAATTGTCAACTATGTAGCTGTGAGCTTATGACTTCATCAAGATG	327
QY	608	CCCTCTGAAAGCAACTCACTGAGAGATGACCTCCCTGGCACTTCACTTGCCTTTG	667
Db	328	CTCTCTGAAAGCAACTCACTGAGAGAGCACTCCCTTGGCACTTCACTTGCCTTTG	387
QY	668	GAGCAGAGCTTGTGCACCACTGTCAATGCTCCCTCTGTAGACGTGTCAAGAGATACA	727
Db	388	GGGGGGGCTTGTGCACCACTGTCAATGCTCCCTCTGTAGATGTGTCAAGAGATATA	447
QY	728	TGAACCTGTGGCCGTGGGCCAGTACAGTAGGGCTGGCCACTGTGCTTAACATGCTCAAG	787
Db	448	TGAACCTGTGGCTTGGGCCAGTACCAAGCGCCGCACTGTGGCCCTAACATGCTCCGAA	507
QY	788	AGGAGGGGCCCGAGCTTCTACAAAGGATCATGCTCTTTTCTCCGCTTGGATTCCT	847
Db	508	AGGAGGGGCCCGAGCTTCTACAAAGGATTCATGCTCTTCTCCGCTTGGAGATCCT	567
QY	848	GGAAAGT 854	
Db	568	GGAAAGT 574	

```

RESULT 11
PCT-US03/14832-406
Sequence 406, Application PC/TUS0314832
GENERAL INFORMATION:
APPLICANT: PHASE-1 Molecular Toxicology, Inc.
APPLICANT: Kier, Larry
APPLICANT: Nolan, Timothy D.
APPLICANT: Sankar, USA
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Liver Inflammation Predictive Genes
FILE REFERENCE: 2874-023PCT
CURRENT APPLICATION NUMBER: PCT/US03/14832
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/379,831
PRIOR FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 406
LENGTH: 674
TYPE: DNA
/

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Db      154 ATGGTTGAGCTGAAGCCCTTGCAGACGTCCTCCACCAATGCTGTGAAGTTCTCTGGGAGCA 213
QY      61  GGCAAGCTGCTGCATGCGAGATCTCATACCTTCTCTGTGATATGCTAAAGTCCGG 120
Db      214 GGCAAGAGCTGTTTGTGCTGACCTGTATCTTTCATGTGACACAGCAAGTCCCG 273
QY      121 TTAAGATCCAAAGAGAAAGTCAAGGGGCAAGTGGCGCTTAAGCAGCCGCAATACCG 180
Db      274 CTGAGATCCAGGGGAGAAACAG3---CGGTCCAGACGGCCCGGCTGTGACGTACCT 330
QY      181 GGTGTGATGGGACCATCTGTGACATGGTGTGATCTAGAGGCCCCGAAAGCTCTACAT 240
Db      331 GGCTGTGGGACCATCTGTGACATGGTGTGATCTAGAGGCCCCGAAAGCTCTACAT 390
QY      241 GGGCTGTGGCGGCTGTGACAGCGCCAAATAGCTTTGCTGTGTCCGCAATGGGCTGTAT 300
Db      391 GGGCTGTGGCGGCTGTGACAGCGCCAAATAGCTTTGCTGTGTCCGCAATGGGCTGTAT 450
QY      301 GATTCTGTCAAGAGTTCTACA---CCAAAGGCTGTAGATGCGCAATGGGAGCCG 357
Db      451 GACTCTGTAAAGAGGTGTACACCCCAAGGCGGCAACTTCAGCTCACTACCTAC 510
QY      358 CTCTAGAGGAGCAGACCAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 417
Db      511 ATTTGGCGGCTGTGACCAAGAGCCATGGCGGTGACTGTGCCAGCCCAAGATGTG 570
QY      418 GTAAAGTCCGATTTCCAGC-----TCAGGCCGGGCTGTAGTGTGTGTGTGTGTGT 468
Db      571 GTAAAGTCCGATTTCCAGCAGCATACCTGTGGGCGATTCAGAGCGACAGAAATATC 630
QY      469 CAAGGACCGTCAATGCTTCAAGACCAATGCCCCGAGAGAGAGGTTCCGGGCTCTGTG 528
Db      631 AGCGGAGATATGAGAGCTTACAGAACCATGGCCAGGAGAGAGAGTCAAGGGCTGTGTG 690
QY      529 AAAGGACCTCTCCCAATGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db      691 AAAGGACCTTGGCCCAATCATAGAGATGCTATGTCACTGTGTGTGTGTGTGTGTGT 750
QY      589 TATGACCTCATCAAGAGTGCCTCTGTAAAGCAACCTCAATGACAGATGACCTCTGTG 648
Db      751 TACGACATCTCTAAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 810
QY      649 CACTTCACTTGTGCTTTGGGAGAGGCTTGTGACCACTGTGTGTGTGTGTGTGTGTGT 708
Db      811 CACTTGTCTGTGCTTTGGAGCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 870
QY      709 GTGTCAAGAGAGATATGATGACTGTGCTGTGCGGCGAGTACAGTACGCTGTGTGT 768
Db      871 GTGTGAAGAGCCGGTATATGACTGTGCTGTGCGGCGAGTACAGTACGCTGTGTGT 930
QY      769 GCCCTTACATGCTCTCAAGAGAGGAGGCGCCGAGCCTTCTAAGAGGTTTCAATGCCCTTC 828
Db      931 ATGATTAAGATGTGGCCAGAGAGGAGGCGCCAGCAGCTTCTAAGAGGTTGAGCCTCTCC 990
QY      829 TTTCTCC 835
Db      991 TGCCTCC 997

```

RESULT 14
US-10-616-865-9

```

; Sequence 9 Application US/10616865
; GENERAL INFORMATION:
; APPLICANT: NEWELL, MARTHA K
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASE
; FILE REFERENCE: VO139.70017US00
; CURRENT APPLICATION NUMBER: US/10/616.865
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 09/277,575
; PRIOR FILING DATE: 1999-03-27
; PRIOR APPLICATION NUMBER: US 60/082,250
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/101,580

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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/094,519
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-616-865-9

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Query Match      44.2%; Score 411; DB 6; Length 1132;
Best Local Similarity 70.5%; Pred. No. 5,4e-108;
Matches 597; Conservative 0; Mismatches 235; Indels 15; Gaps 3;

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QY      1 ATGGTTGAGCTGAAGCCCTTGCAGACGTCCTCCACCAATGCTGTGAAGTTCTCTGGGAGCT 60
Db      154 ATGGTTGAGCTGAAGCCCTTGCAGACGTCCTCCACCAATGCTGTGAAGTTCTCTGGGAGCA 213
QY      61  GGCAAGCTGCTGCATGCGAGATCTCATACCTTCTCTGTGATATGCTAAAGTCCGG 120
Db      214 GGCAAGAGCTGTTTGTGCTGACCTGTATCTTTCATGTGACACAGCAAGTCCCG 273
QY      121 TTAAGATCCAAAGAGAAAGTCAAGGGGCAAGTGGCGCTTAAGCAGCCGCAATACCG 180
Db      274 CTGAGATCCAGGGGAGAAACAG3---CGGTCCAGACGGCCCGGCTGTGACGTACCT 330
QY      181 GGTGTGATGGGACCATCTGTGACATGGTGTGATCTAGAGGCCCCGAAAGCTCTACAT 240
Db      331 GGCTGTGGGACCATCTGTGACATGGTGTGATCTAGAGGCCCCGAAAGCTCTACAT 390
QY      241 GGGCTGTGGCGGCTGTGACAGCGCCAAATAGCTTTGCTGTGTCCGCAATGGGCTGTAT 300
Db      391 GGGCTGTGGCGGCTGTGACAGCGCCAAATAGCTTTGCTGTGTCCGCAATGGGCTGTAT 450
QY      301 GATTCTGTCAAGAGTTCTACA---CCAAAGGCTGTAGATGCGCAATGGGAGCCG 357
Db      451 GACTCTGTAAAGAGGTGTACACCCCAAGGCGGCAACTTCAGCTCACTACCTAC 510
QY      358 CTCTAGAGGAGCAGACCAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 417
Db      511 ATTTGGCGGCTGTGACCAAGAGCCATGGCGGTGACTGTGCCAGCCCAAGATGTG 570
QY      418 GTAAAGTCCGATTTCCAGC-----TCAGGCCGGGCTGTAGTGTGTGTGTGTGTGT 468
Db      571 GTAAAGTCCGATTTCCAGCAGCATACCTGTGGGCGATTCAGAGCGACAGAAATATC 630
QY      469 CAAGGACCGTCAATGCTTCAAGACCAATGCCCCGAGAGAGAGGTTCCGGGCTCTGTG 528
Db      631 AGCGGAGATATGAGAGCTTACAGAACCATGGCCAGGAGAGAGTCAAGGGCTGTGTG 690
QY      529 AAAGGACCTCTCCCAATGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db      691 AAAGGACCTTGGCCCAATCATAGAGATGCTATGTCACTGTGTGTGTGTGTGTGTGT 750
QY      589 TATGACCTCATCAAGAGTGCCTCTGTAAAGCAACCTCAATGACAGATGACCTCTGTG 648
Db      751 TACGACATCTCTAAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 810
QY      649 CACTTCACTTGTGCTTTGGGAGAGGCTTGTGACCACTGTGTGTGTGTGTGTGTGTGT 708
Db      811 CACTTGTCTGTGCTTTGGAGCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 870
QY      709 GTGTCAAGAGAGATATGATGACTGTGCTGTGCGGCGAGTACAGTACGCTGTGTGT 768
Db      871 GTGTGAAGAGCCGGTATATGACTGTGCTGTGCGGCGAGTACAGTACGCTGTGTGT 930
QY      769 GCCCTTACATGCTCTCAAGAGAGGAGGCGCCGAGCCTTCTAAGAGGTTTCAATGCCCTTC 828
Db      931 ATGATTAAGATGTGGCCAGAGAGGAGGCGCCAGCAGCTTCTAAGAGGTTGAGCCTCTCC 990
QY      829 TTTCTCC 835

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Db 991 TGCTCC 997

RESULT 15

US-10-743-643-171
; Sequence 171, Application US/10743643
; GENERAL INFORMATION:
; APPLICANT: Woolf et al.
; TITLE OF INVENTION: Nucleic acid and amino acid sequences involved in pain
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/743,643
; PRIORITY FILING DATE: 2003-12-22
; FILE REFERENCE: 17633/2005
; PRIORITY FILING DATE: 2002-07/14
; NUMBER OF SEQ ID NOS: 2605
; SOFTWARE: Perl script
; SEQ ID NO 171
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Refseq / NM_022803
; DATABASE ENTRY DATE: 2001-03-09
US-10-743-643-171

Query Match 44.2%; Score 411; DB 6; Length 1182;

Best Local Similarity 70.5%; Pred. No. 5,5e-108;

Matches 597; Conservative 0; Mismatches 235; Indels 15; Gaps 3;

QY 1 ATGTTGGGTTCAAGGCCAAGATGTGCCCCCTACTGCCCAGTGTGAAGTTTCTTGAGGCT 60
Db 204 ATGTTGGACTGAAGCTTTCAGAGTGTCTCCCAAGATGCTGTGAAGTTCTTGAGGCA 263
QY 61 GGACAGCTGCTGATGAGATGATCATCACTTCTCTGATACTGTAAAGTCCGG 120
Db 264 GGACAGAGCTGTTTGTGCTGACCTGTTTCCACTGAGACAGCAAGTCCGC 323
QY 121 TTACAGATCCAAAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCACTACCCG 180
Db 324 CTGCAGATCCAGGGGAGAACAGG---CGGTCCAGAGGCGCGCTCGTGCAGTACGAT 380
QY 181 GGTGTGATGGGACACATCTGACATGAGTGTGCTGAGGGCCCGGAAAGCTCTCAAT 240
Db 381 GGTGTGATGGGACACATCTGACATGAGTGTGCTGAGGGCCCGGAAAGCTCTCAAT 440
QY 241 GGGCTGTGTCGCGGCTGCAAGGCCAATGAGCTTGTCTGTGCGATGAGCTGTAT 300
Db 441 GGGCTGTGTCGCGGCTGCAAGGCCAATGAGCTTGTCTGTGCGATGAGCTGTAT 500
QY 301 GATTCTGTCAACAGTTCTTACA---CCAAGGCTCTGAGCATGCGAGATTGGAGCGC 357
Db 501 GACTCCGTCAAGCAGGTGACACCCCAAGGCGGAGCACTTCAAGCTCACTACCCG 560
QY 358 CTCTAGCAGCAGCAGCAGCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 417
Db 561 ATTTTGGCGGTGACACCAAGGAGCATGCGGTGACCTGTGCTGCTGCTGCTGCTGCTG 620
QY 418 GTAAAGTCCGATTCAGC-----TGAAGCCGCGGTGAGGTGTGCGAGATAC 468
Db 621 GTGAAGTCCGATTCAGC-----TGAAGCCGCGGTGAGGTGTGCGAGATAC 680
QY 469 CAAGACCGCTCAATGCTTACAAAGCATTGCGCCGAGAGAGAGGTTCCGGGCTCTGG 528
Db 681 AGCGGACATATGAGCGCTTACAAAGCATTGCGCCGAGAGAGAGGTTCCGGGCTCTGG 740
QY 529 AAAAGGACCTTCTCCCAATGTCTGTATGTGCACTTGTCACTGTGCTGAGCTGTGAC 588
Db 741 AAAGGAACTTTGCCCAATGTCTGTATGTGCACTTGTCACTGTGCTGAGGTGTGAC 800
QY 589 TATGACCTATCAAGGATGCTCTCTGAAAGCCTCATGAGAGATGACCTTCTTGC 648
Db 801 TAGGATCTCTCAAGGAGAGAGTGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTG 860

QY 649 CACTTCACTTGTGCTTGGGGCAGGCTTGTGACCACTGTCAATGCTTCCCTGTAGAC 708
Db 861 CACTTGTGCTTGTGAGCCGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 920
QY 709 GTGTCAAGCAGATATCACTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 768
Db 921 GTGTCAAGCAGATATCACTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 980
QY 769 GCCCTTACATGCTTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
Db 981 ATGATTAAGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1040
QY 829 TTTCTCC 835
Db 1041 TGCTCC 1047

Search completed: February 4, 2004, 20:16:37
Job time : 415 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 17:52:58 / Search time 2412 Seconds

(without alignments)
9371.129 Million cell updates/sec

Title: US-09-884-814-2

Sequence: 1 atgcttggtcctcagagccac.....cccgagaggtcccttcgca 930

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba.*
2: em_estba.*
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29: em_estba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	781.2	84.0	3641	AK054060	AK054060 Mus muscu
2	779.6	83.8	3964	AK035298	AK035298 Mus muscu
3	731.4	78.6	782	BF974251	BF974251 602243895
4	725	78.0	807	BF974251	BF974251 602243895

Result No.	Score	Query Match	Length	ID	Description
5	702.6	75.5	739	CA944705	CA944705 UT-CF-FNO
6	702.2	75.5	932	B1258707	B1258707 602969874
7	684.2	73.6	752	BM015784	BM015784 603642048
8	672.8	72.3	937	B1249501	B1249501 6029292916
9	672.4	72.3	1201	AL542338	AL542338 AL542338
10	659	70.9	1201	AL581378	AL581378 AL581378
11	652.4	70.2	938	B1692548	B1692548 603343091
12	647.6	69.6	1125	AL575087	AL575087 AL575087
13	640.6	68.9	859	B1904624	B1904624 602244382
14	635.4	68.3	1201	B1904624	B1904624 603166439
15	634.6	68.2	1201	AL552549	AL552549 AL552549
16	633.8	68.2	1073	AL555585	AL555585 AL555585
17	630.6	67.8	650	AL133329	AL133329 HA1932_Hu
18	630.6	67.8	1201	AL523574	AL523574 AL523574
19	626	67.3	709	BG284068	BG284068 602407385
20	624	67.1	1167	BX421118	BX421118 BX421118
21	618	66.5	766	BG976754	BG976754 602845813
22	617.2	66.4	1201	AL516805	AL516805 AL516805
23	616.4	66.3	644	BG825731	BG825731 602747049
24	613.4	66.0	997	BX343473	BX343473 BX343473
25	610.8	65.7	1065	BG754934	BG754934 602711629
26	609.6	65.5	753	BG513450	BG513450 601316120
27	608.6	65.4	754	BG340587	BG340587 602462157
28	606.2	65.2	794	BG68126	BG68126 602635587
29	603.4	64.9	1201	BX375133	BX375133 BX375133
30	602.6	64.8	1201	AL559843	AL559843 AL559843
31	600.8	64.6	882	BX384593	BX384593 BX384593
32	596.6	64.2	701	AL430170	AL430170 me41808.Y
33	594.6	63.9	1060	AL555584	AL555584 AL555584
34	594.4	63.9	896	BG341258	BG341258 602463324
35	590.4	63.5	592	BX343474	BX343474 BX343474
36	589.2	63.4	995	BES14976	BES14976 601317285
37	588.2	63.4	905	BES18001	BES18001 602100115
38	586.8	63.1	1177	B0050380	B0050380 AGENCOURT
39	583.2	62.7	684	CB446089	CB446089 697877.MA
40	580.8	62.5	1201	AL563224	AL563224 AL563224
41	580.4	62.4	1196	AL562228	AL562228 AL562228
42	579.4	62.3	859	BG972368	BG972368 602841319
43	576.2	62.0	697	BG965001	BG965001 602831635
44	576.2	62.0	818	B1904048	B1904048 603165559
45	572.2	61.5	1201	AL516806	AL516806 AL516806

ALIGNMENTS

RESULT 1
AK054060
LOCUS
DEFINITION
Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:182001518 Product:uncoupling protein 2, mitochondrial, full insert sequence.

ACCESSION
AK054060.1 GI:26343968
VERSION
AK054060.1
KEYWORDS
Mus musculus (house mouse)
SOURCE
HTC, CAP trapper.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
1
Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
11042159

REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagacka, S., Sasaki, N., Carninci, P., Komori, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, M., Ozawa, K., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, K., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE PUBMED REFERENCE AUTHORS	20530913 11076861 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Komori, H., Aachi, J., Fukuda, S., Aizawa, K., Ozawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamahara, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Pleischmann, W., Gassterland, T., Gissi, C., King, B., Kochiwa, H., Kueh, P., Lewis, S., Matsuo, Y., Nikaido, I., Pease, G., Tomita, M., Quackenbush, J., Schriml, L. M., Staudt, F., Suzuki, R., Wagner, D., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Wetz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohzuki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE PUBMED REFERENCE AUTHORS	21085660 11217851 5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE AUTHORS	6 (bases 1 to 3641) Aach, U., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T., Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, A., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers

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BASE COUNT	791 a 1075 c 934 g 841 t
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Best Local Similarity	90.0%; Pred. No. 5.2e-189;
Matches 837; Conservative	0; Mismatches 93; Indels 0; Gaps 0;
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61	GGCACAGCTGCTGATGACATGATCTATCACTCTTCTGATGATCTGTAAGTCCG 180
429	GGGACAGCTGCTGATGATGATCTATCTATCTCTCTGATGATCTGTAAGTCCG 240
121	TTCAGATTCAGAGAAAGTCAGGGGCGATGGCGGTACAGCCAGCCGACATACCG 300
489	CTGCAATCCAAAGGAGAGTCAGGGGCTAGTGGACCGACCGACCGCCAGTACCT 360
181	GGTGTATGGGACCATCTGACATGTCGATGTCGATGTCGATGTCGATGTCGATG 420
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609	GGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 600
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361	CTACAGGACGACACACAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 780
729	CTGACAGGACGACACACAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 840
421	AGGTCGATTCAGGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
789	AGGTCGATTCAGGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 960
481	AATGCTTCAACAGTTCATCAACAGGAGCTCTGACATGTCGATGTCGATGTCGAT 1020
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909	CCAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1200
601	AAGATGCTCTCTGAAAGCACTGACATGATGATGATGATGATGATGATGATGATG 1260

Db		966	AAAAGTACTCTTCGTAAGAACCACCTCATGACAGATGACCTCCGTGGCACTTCACTTCT	1028
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Db		1029	GCTTCGCGGGCGGGCTTTGTGCACACCGTATGCGCTCCCTGTGTGATGTGGTCAAAGC	1088
QY		721	AGATACATAA CTCTGCCCTTGGGCGCAGTACAGTAGCGCTGGCCACCTGTGCCCTTACATG	780
Db		1089	AGATTACATAACTCTGCTCTTGGGCGCACATGACAGCGCAGTGTACATGTCGCTTACATG	1148
QY		781	CTCCAGAGAGAGGAGCGGCCCGGAGCCTTTCTPAAAGGTTATGCGCTCTTTTCTCCGCTTG	840
Db		1149	CTCCGGAAGAGAGGAGCCCCGGCGCTTCTTCAAGGGGTTTCA TGCTTCTTCTCCGCTTG	1208
QY		841	GGTTCTCGAAGCTGTGTATGTTGTGTGACCACTATAGAGAGTGAAGAGCGCTCAATGACT	900
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Db		1269	GCCTACCAATCTCGGAGGACACTTTTCTGA	1298
RESULT 2				
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LOCUS		3964 bp	mRNA	linear
DEFINITION		Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:195001110 product:uncoupling protein 2, mitochondrial, full insert sequence.		
ACCESSION		AK035298		
VERSION		AK035298.1	GI:26330581	
SOURCE		HTC; CAP trapper.		
ORGANISM		Mus musculus (house mouse)		
REFERENCE				
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.		
TITLE		Carninci, P. and Hayashizaki, Y		
JOURNAL		High-efficiency full-length cDNA cloning		
MEDLINE		Meth. Enzymol. 303, 19-44 (1999)		
PUBMED		99279253		
REFERENCE		10349636		
AUTHORS				
TITLE		Carninci, P., Shibata, Y., Hayaasu, N., Sugihara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Kuramatsu, M., and Hayashizaki, Y.		
JOURNAL		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
MEDLINE		Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED		20499374		
REFERENCE		11042159		
AUTHORS				
TITLE		Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitamura, T., Teshitiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Hatada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Itawa, M., Ohara, E., Washiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawaj, J., Okazaki, Y., Muramatsu, K., Inoue, Y., Kita, A. and Hayashizaki, Y.		
RKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer				
Genome Res. 10 (11), 1757-1771 (2000)				
Journal 20530913				
PUBMED 11076861				
REFERENCE				
AUTHORS				
Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komoto, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Komodo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasuyawa, T., Saito, R., Kato, C., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kushl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pezole, G., Quackenbush, J., Scrimm, L.M., Stebbins, F., Suzuki, R., Tomita, M., Wagner, D., Washio, T., Sakai, K., Oikido, T., Furuno, M., Aono, H.,				

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	
AUTHORS	5
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 3964)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M., Koyama,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishii,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeba,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/ Location/Qualifiers
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BASE COUNT 861 a 1158 c 1021 g 904 t
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Query Match 83.8%; Score 779.6; DB 11; Length 3964;
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 1023 GCTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1082
 721 AGATTCATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 1083 AGATTCATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1142
 781 CTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 1143 CTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1202
 841 GGTTCCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 1203 GGTTCCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1262
 901 GGTTCCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930
 1263 GGTTCCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1252

RESULT 3
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 LOCUS
 DEFINITION
 602243895F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335167 5',
 mRNA sequence.
 ACCESSION
 BF974251
 VERSION
 BF974251.1 GI:12341466
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 782)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM1205 row: m column: 24
 High quality sequence stop: 780.
 Location/Qualifiers

FEATURES

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 /notes="Organ: B-cells; Vector: pORF7; Site: 1; XhoI;
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 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACAG(G). Size-selected 500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT

ORIGIN
 159 a 239 c 219 g 165 t

Query Match 78.6%; Score 731.4; DB 10; Length 782;
 Best Local Similarity 99.7%; Pred. No. 1.3e-176;
 Matches 743; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

55 GGGGCTGGGACAGCTGCTGTCATCGCATCTTCATCACTTCTTCTGTAATCTGTA 114
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 174 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 233
 122 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 181
 234 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 293
 182 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 241
 294 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 353
 242 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 301
 354 GTCGGTTACAGATCCAA-GGAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 413

Db	302	CCGCTCTCTAGAGGACAGACCA	CAGGTGCCCTGCTGTGTGCTGTGTGCCCACTCCAGGGA	361
QY	414	TGTGTAAAGSTCCGATTCC	AAGCTCAGGCCCGGGCTGAGGTGTGAGATATCCAAAG	473
Db	362	TGTGTAAAGSTCCGATTCC	AAGCTCAGGCCCGGGCTGAGGTGTGAGATATCCAAAG	421
QY	474	CACCGTCATGCTCTACAAG	ACCATTTGCCGAGAGAAAGGTTCCGGGGGCTGTGAAAAG	533
Db	422	CACCGTCATGCTCTACAAG	ACCATTTGCCGAGAGAAAGGTTCCGGGGGCTGTGAAAAG	481
QY	534	GACCTTCCCATGTTGTGCTG	TAAAGCCATTGTCACTGTGTGACTGTGACTTGA	593
Db	482	GACCTTCCCATGTTGTGCTG	TAAAGCCATTGTCACTGTGTGACTGTGACTTGA	541
QY	594	CCTCATCAAGATGCGCTCTG	AAAAGCCAACTTCATGACATGACCTCCCTTGCACTT	653
Db	542	CCTCATCAAGATGCGCTCTG	AAAAGCCAACTTCATGACATGACCTCCCTTGCACTT	601
QY	654	CACCTTGTGCTTTGGGGCAG	GGCTTGTGCACCACTGTATGCTCTCCCTGTGAGAGTGT	713
Db	602	CACCTTGTGCTTTGGGGCAG	GGCTTGTGCACCACTGTATGCTCTCCCTGTGAGAGTGT	661
QY	714	CAGAGCAGATATCAATGA	ACTCTGCCCTGGGCAATACAGTAAAGGCTGGGCACTGGGCCCT	773
Db	662	CAGAGCAGATATCAATGA	ACTCTGCCCTGGGCAATACAGTAAAGGCTGGGCACTGGGCCCT	721
QY	774	TACCATGCTCAGAAAGGA	GGGCC 798	
Db	722	TACCATGCTCAGAAAGGA	GGGCC 746	

FEATURES
 source
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: c9abbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://lcm1703.row.1.column.22>
 High quality sequence step: 788.
 Location/Qualifiers
 1..807

[illegible]

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source
 1..739
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-afr-m-14-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_id="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two
 normalized Human lung epithelial cell libraries (EM1 and
 DU1) The library was subtracted according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG LIB=UI-CF-FNO
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG_SEQ=CTGCTCAGGT"
 BASE COUNT 155 a 197 c 223 g 163 t 1 others
 ORIGIN
 Query Match 75.5%; Score 702.6; DB 14; Length 739;
 Best local similarity 97.9%; Pred. No. 3.1e-169;
 Matches 711; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

460 CGAGATACCAAGACCGTCATAGCTACAGACCATTCGCCGAGAGAGGATTCGG 519
 439 CGGATATACCAAGACCGTCATAGCTACAGACCATTCGCCGAGAGAGGATTCGG 380
 520 GGCCTCTGGAAGGAGACCTCTCCCAATGTTGCTGTAAATGCCATGTGCACTGTGCTGAG 579
 379 GGCCTCTGGAAGGAGACCTCTCCCAATGTTGCTGTAAATGCCATGTGCACTGTGCTGAG 320
 580 CTGTGACCTTATGACCTCATCAAGATGACCTCTCCGAAAGCAACCTCATGACAGATGAC 639
 319 CTGTGACCTTATGACCTCATCAAGATGACCTCTCCGAAAGCAACCTCATGACAGATGAC 260
 640 CTCCCTTGGCACTTCACTTCTGCTCTTGGGCGAGGCTTTCGACCATGTGATGCTCC 639
 259 CTCCCTTGGCACTTCACTTCTGCTCTTGGGCGAGGCTTTCGACCATGTGATGCTCC 200
 700 CCTGTAGACGTGTGACAGAGATATACATGACCTGACCTGAGGACATACATGACGCT 759
 199 CTTGTAGACGTGTGACAGAGATATACATGACCTGACCTGAGGACATACATGACGCT 140
 760 GGCACTGTGCTCCCTTACCATGCTCTCCAGAGAGAGGAGGAGGCTTCTTCAAGAGGCTTC 819
 139 GGCACTGTGCTCCCTTACCATGCTCTCCAGAGAGAGGAGGAGGCTTCTTCAAGAGGCTTC 80
 820 ATGCCCTCTTCTCCGCTGAGGCTTCTCCGAGAGAGGAGGAGGCTTCTTCAAGAGGCTTC 879
 79 ATGCCCTCTTCTCCGCTGAGGCTTCTCCGAGAGAGGAGGAGGCTTCTTCAAGAGGCTTC 20
 880 CTGAAA 885
 19 CAAAA 14

RESULT 6
 LOCUS B1258707
 DEFINITION 602969874F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109050 5',
 mRNA sequence.
 ACCESSION B1258707
 VERSION B1258707.1 GI:14815328
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 932)
 AUTHORS NIH-MGC http://imgc.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 http://image.llnl.gov
 Plate: L1AM1264 row: d column: 19
 High quality sequence stop: 799.
 Location/Qualifiers
 1..932
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5109050"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_id="NIH MGC 12"
 /note="Organ: cervix; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life

BASE COUNT 172 a 289 c 250 g 221 t
 ORIGIN
 Query Match 75.5%; Score 702.2; DB 12; Length 932;
 Best Local Similarity 96.9%; Pred. No. 4,4e-169;
 Matches 780; Conservative 0; Mismatches 18; Indels 7; Gaps 6;

133 GGAAGAACTCAGGGGCGGCTGCGGCTACAGCCAGCGGCCCA-GTACCGGGGTGTATGAG 191
 1 GGAAGAACTCAGGGGCGGCTGCGGCTACAGCCAGCGGCCCAAGTACCGGGGTGTATGAG 60
 192 CACCAATTCGACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
 61 CACCAATTCGACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 252 CGGCTGCAAGGCGCCAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
 121 CGGCTGCAAGGCGCCAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 312 ACAGTTCTACACCAAGGCGCTCTGAGCATGCGAGCATTTGGAGCGGCTCTCTACAGGCA 371
 181 ACAGTTCTACACCAAGGCGCTCTGAGCATGCGAGCATTTGGAGCGGCTCTCTACAGGCA 240
 372 CACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
 241 CACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 432 CCAAGGCTGAGGCGGCGGCTGAGGCTGCTGAGGATACCAAGACCGCTCATGCTTACAA 491
 301 CCAAGGCTGAGGCGGCGGCTGAGGCTGCTGAGGATACCAAGACCGCTCATGCTTACAA 360
 492 GACCAATTCGACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
 361 GACCAATTCGACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 550 GCTGCTGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
 421 GCTGCTGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 610 CTCCTGAAAGCCAACTCATGACAGATGACCTCCCTGCACTTCACTTCTGCTTGGG 669
 481 CTCCTGAAAGCCAACTCATGACAGATGACCTCCCTGCACTTCACTTCTGCTTGGG 540
 670 GCAAGGCTTCTGC-AACAGCTGATGCGCTCCCTGCTGATGAGCGTCAAGAGATACAT 728
 541 GCAAGGCTTCTGC-AACAGCTGATGCGCTCCCTGCTGATGAGCGTCAAGAGATACAT 600
 729 GAACTCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
 601 GAACTCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 788 AGAGAGGCGGCGGCGGCTTCTACAAAGGCTTATGCTCTTCTGCTGCTGCTGCTGCT 847
 661 AGAGAGGCGGCGGCGGCTTCTACAAAGGCTTATGCTCTTCTGCTGCTGCTGCTGCT 720
 848 GGAAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
 721 GGAAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 906 CACTTCCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
 781 CACTTCCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 805

RESULT 7
 LOCUS 5M015784
 DEFINITION 603642048F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5418106 5',
 mRNA sequence.
 ACCESSION 5M015784
 VERSION 5M015784.1 GI:16530138
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC
 TITLE NIH-MGC
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL2066 row: P column: 11
 High quality sequence stop: 752.
 Location/Qualifiers
 1..752
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5418106"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_87"
 /note="Organ: Breast; Vector: pCMV-Sport6; Site: 1; NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 151 a 229 c 203 g 169 t
 ORIGIN
 Query Match 73.6%; Score 684.2; DB 12; Length 752;
 Best Local Similarity 99.4%; Pred. No. 1.6e-164;
 Matches 697; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1 ATGTTGGGTTTCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 51 ATGTTGGGTTTCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 110
 61 GGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 111 GGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 170
 121 TTACAGATCCAAAGGAAAGTCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 171 TTACAGATCCAAAGGAAAGTCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
 181 GGTGATGAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 231 GGTGATGAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290
 241 GGGCTGTTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 291 GGGCTGTTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
 301 GATTCTGTCAAAAGCTTTACACCAAGGCTCTGAGATGCGACATTTGGAGCGGCTC 360
 351 GATTCTGTCAAAAGCTTTACACCAAGGCTCTGAGATGCGACATTTGGAGCGGCTC 410
 361 CTAGAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 411 CTAGAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
 421 AAGTCCGATTTCAAGCTCAGGCGGCGGCTGAGAGTGTGCGAGATACCAAGACCGCTC 480
 471 AAGTCCGATTTCAAGCTCAGGCGGCGGCTGAGAGTGTGCGAGATACCAAGACCGCTC 530
 481 AATGCTTACAGACCATTTGCCGAGAGGAGGCTTCGGGGCTCTTGGAAGGACCTCT 540

Db 531 AATGCTACAAAGCCATTGGCCCGAGAGAGGATTCGGGGGCTCTGAAAGAGGACCTCT 590
 541 CCCAATGTTGCTGTATAGCATTTGCACTGTGCTGAGTGTGACCTATGACCTCATC 600
 Db 591 CCCAATGTTGCTGTATAGCATTTGCACTGTGCTGAGTGTGACCTATGACCTCATC 650
 Qy 601 AAGATGCTCTCTGAAAGCCAACTGATGACATGACCTCTGCTGCACTTCACTTCT 660
 Db 651 AAGATGCTCTCTGAAAGCCAACTGATGACATGACCTCTGCTGCACTTCACTTCT 710
 Qy 661 GCC-TTGGGGGAGGCTTCTGCACTGCTGATGCTGCTCC 700
 Db 711 GCTTTTGGGGGAGGCTTCTGCACTGCTGATGCTGCTCC 751

RESULT 8 927 bp mRNA linear EST 17-JUL-2001
 B1248501 602929216F1 NCI_CGAP_Mams Mus musculus cDNA clone IMAGE:5148915 5',
 LOCUS B1248501 GI:14794652
 DEFINITION mRNA sequence.
 ACCESSION B1248501
 VERSION B1248501.1 GI:14794652
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 927)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-rtm.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM11367 row: P column: 04
 High quality sequence stop: 919.
 Location/Qualifiers

FEATURES
 source 1..927
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:5148915"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DHI0B"
 /clone_1ib="NCI CGAP Mams"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; site 2: NciI; Cloned unidirectionally. Primer: Oligo dT. library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 180 a 296 c 248 g 203 t
 ORIGIN
 Query Match 72.3%; Score 672.8; DB 12; Length 927;
 Best Local Similarity 88.3%; Pred. No. 1.5e-161;
 Matches 765; Conservative 0; Mismatches 97; Indels 4; Gaps 3;

Qy 61 GGCAAGCTGCTGTCATCGCAATCTCATCACTTCTCTGATGATGCTAAAGTCGG 120
 Db 7 GTGCGAGCTGCTGCTGATGCAATCTCATCACTTCTCTGATGATGCTAAAGTCGG 66
 Qy 121 TTACAGATCCAAAGAAAGTACGGGGCAGTCCGCTACAGCCAGCCAGTACCGC 180
 Db 67 CTGCAATCCAAAGGAGACTCAAGGCTAGTGGGACCGAGCCAGCCAGTACCGT 126

Qy 181 GGTGTGATGGGACACATTCTGACATGTGCTGACTAGAGGAGCCCGGAGCCTCTACAT 240
 Db 127 GAGCTTCTGGATACATCTTACATAGTGTGGACCTAGAGGTCCAGCAGCCTCTACAT 186
 Qy 241 GGGCTGTTGCCGAGCTTCAGCCGCAATAGACTTTGCTCTGTGCTGCTGCTGAT 300
 Db 187 GGGCTGTTGCCGAGCTTCAGCCGCAATAGACTTTGCTCTGTGCTGCTGCTGAT 246
 Qy 301 GATTCTGTAAACAATTCTTACACCAAGGCTCTGAGCATGACATTGGAGCCGCTC 360
 Db 247 GACTCTGTAAACAATTCTTACACCAAGGCTCTGAGCATGACATTGGAGCCGCTC 306
 Qy 361 CTAGCAGCAGCAGCAGCAGTGCCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 420
 Db 307 CTGGCAGTACAGCAGCAGTGCCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 366
 Qy 421 AAGTCCGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 480
 Db 367 AAGTCCGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 426
 Qy 481 AATGCTTACAGACATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 540
 Db 427 GAGCTTACAGACATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 486
 Qy 541 CCCAATGTTGCTGTATAGCATTTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
 Db 487 CCCAATGTTGCTGTATAGCATTTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 Qy 600 CAAGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCTGCTGCTGCTGCTGCT 659
 Db 547 CAAGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTCTGCTGCTGCTGCTGCT 606
 Qy 660 TGCTTTGGGGGAGGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
 Db 607 TGCTTTGGGGGAGGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 Qy 720 GAGTATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
 Db 667 GAGTATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 Qy 780 GCTTCAGAGAGAGGAGGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
 Db 727 GCTTCAGAGAGAGGAGGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 Qy 840 GGGTCTCTGGAAGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
 Db 787 GGGTCTCTGGAAGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 Qy 900 TGCTTCGACTTCCGAGAGGCTGCTCT 925
 Db 844 TGCTTCGACTTCCGAGAGGCTGCTCT 869

RESULT 9 1201 bp mRNA linear EST 12-MAY-2003
 AL542338 Homo sapiens PLACENTA Homo sapiens cDNA clone CS05D0107H17
 LOCUS AL542338
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION AL542338
 VERSION AL542338.2 GI:30547386
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B.; Gruber, C.; Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12874284.
 Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3923.f. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D050YK17-3-PRIME, mRNA sequence.
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D050YK17-3-PRIME

FEATURES

Location/Qualifiers
 1. 1201

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D050YK17"
 /issue_type="PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo (dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT 253 a 340 c 316 g 266 t 26 others
 ORIGIN

Query Match 72.3% Score 672.4; DB 9; Length 1201;
 Best Local Similarity 92.5%; Pred. No. 2.2e-161;
 Matches 736; Conservative 21; Mismatches 32; Indels 7; Gaps 5;

1 ATGTTGGGTTCAAGGCGACAGATGTCCTTCACTGCACTGTAAGTTCTTGGAGCT 60
 411 ATGTTGGGTTCAAGGCGACAGATGTCCTTCACTGCACTGTAAGTTCTTGGAGCT 470
 61 GGCAAGCTGCTGATGCGAGATCTCATACCTTCTGATGTAAGTCCGG 120
 471 GGCAAGCTGCTGATGCGAGATCTCATACCTTCTGATGTAAGTCCGG 530
 121 TTACAGATCCAAAGAGAAAGTCAAGGCGCAGTGCCTCAAGCGCCAGTACCG 180
 531 TTACAGATCCAAAGAGAAAGTCAAGGCGCAGTGCCTCAAGCGCCAGTACCG 590
 181 GGTGTGATGGGACCATTTCTGACATGATGCTGTAAGGCGCCCAAGCTCTTCAAT 240
 591 GGTGTGATGGGACCATTTCTGACATGATGCTGTAAGGCGCCCAAGCTCTTCAAT 650
 241 GGGCTGGTGGCGGCTGAGCGGCAATGAGCTTGGCTCTGCGCATCGGCTGTAT 300
 651 GGGCTGGTGGCGGCTGAGCGGCAATGAGCTTGGCTCTGCGCATCGGCTGTAT 710
 301 GATTCTGTCAACAGTTTCAACCAAGGCTCTGAGCATGCGCATTTGAGAGCGCTTC 360
 711 GATTCTGTCAACAGTTTCAACCAAGGCTCTGAGCATGCGCATTTGAGAGCGCTTC 770
 361 CTAGAGAGGAGACCAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 771 CTAGAGAGGAGACCAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
 421 AAGTCCGATTCGAAGCTCAAGGCTCGGCTGAGTGTGAGAGTACCAAGGACCGTC 480
 831 AAGTCCGATTCGAAGCTCAAGGCTCGGCTGAGTGTGAGAGTACCAAGGACCGTC 890
 481 AATGCTTCAACAGATTCGCGGAGAGAGAGGTTCCGGGGCTCTGAAAGGAGACTCT 540
 891 AATGCTTCAACAGATTCGCGGAGAGAGAGGTTCCGGGGCTCTGAAAGGAGACTCT 950
 541 CCCAATGTTGCTGTAAGCATTTGCACTGTGCTGAGTCTGAGTCTGAGTCTGAGTCT 599
 951 CCCAATGTTGCTGTAAGCATTTGCACTGTGCTGAGTCTGAGTCTGAGTCTGAGTCT 1010
 600 CAAAGATGCTCTCTGAAAGGCAAGCTCATG-ACAGATGAGCTCTCTGCACTTCACT 658
 1011 CAAAGATGCTCTCTGAAAGGCAAGCTCATG-ACAGATGAGCTCTCTGCACTTCACT 1070

659 CTGCTTTGGGAGAGGCTTCTGACACACTGTGATGCTTCCCTTGTAAAGCTGTCAAGA 718
 1071 CTGCTTTGGGAGAGGCTTCTGACACACTGTGATGCTTCCCTTGTAAAGCTGTCAAGA 1129
 719 CGAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 778
 1130 CG-GRDMAAGAACTTGGCTTGGGSAK--ACARTAGAGTGGCMCTKTKCCTTCAAT 1185
 779 TGTCTCAAGAGAGG 794
 1186 TGTCTCAAGAGAGG 1201

RESULT 10
 AL581378/c 1201 bp mRNA linear EST 01-JUN-2003
 LOCUS
 DEFINITION
 AL581378 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
 clone CS0D050YK17-3-PRIME, mRNA sequence.
 AL581378
 VERSION
 KEYWORDS
 EST.
 AL581378.2 GI:31319618

ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 16, 2001 this sequence version replaced gi:12948318.
 CONTACT
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5666.t For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D050YK17-3-PRIME, mRNA sequence.
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D050YK17-3-PRIME

FEATURES

Location/Qualifiers

1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D050YK17"
 /issue_type="B CELLS (RAMOS CELL LINE)"
 /cell_line="RAMOS CELL LINE"
 /clone_id="Homo sapiens B CELLS (RAMOS CELL LINE)"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo (dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT 282 a 250 c 377 g 207 t 85 others
 ORIGIN

Query Match 70.9% Score 659; DB 9; Length 1201;
 Best Local Similarity 97.6%; Pred. No. 5.9e-158;
 Matches 696; Conservative 11; Mismatches 2; Indels 4; Gaps 4;

219 GGGCCCCGAGAGCTCTACAAATGGGCTGTGCGGCTGAGCGGCAATGAGCTTGC 278
 1073 VGGGCCCCGAGAGCTCTACAAATGGGCT-GTGCGGCTGAGCGGCAATGAGCTTGC 1016
 279 CTCTGTCCGATCGGCTGTGATGATTTGTCAACAGTTTCAACAGAGGCTCTGAGCA 338
 1015 CTCTGTCCGATCGGCTGTGATGATTTGTCAACAG-TTCAACAGAGGCTCTGAGCA 957
 339 TCCAGCATTTGGAGAGCGGCTCTGAGAGG-CAGACCAAGAGTGGCTGCTGAGCTG 397

```

Db      956 TGCACGATTGGAGAGCGCTCTTACGACGCGACAGACAGAGTCCCTGCTGGCTG 897
QY      398 TGGCCCAAGCCCAAGATGTGTGAAGGTCCGATTCCAGCTAGGCCCGGGCTGAGGTG 457
Db      896 TGGCCCAAGCCCAAGATGTGTGAAGGTCCGATTCCAGCTAGGCCCGGGCTGAGGTG 837
QY      458 GTGGAGATACCAAGACCGTCAATGCTTACAGACCAATGCCGAGAGAGAGGTTCC 517
Db      836 GTGGAGATACCAAGACCGTCAATGCTTACAGACCAATGCCGAGAGAGGTTCC 777
QY      518 GGGGCTCTGAGAAAGGAGCTTCCCAATGTGTCTGTAATGCAATGTCACTGTGCTG 577
Db      776 GGGGCTCTGAGAAAGGAGCTTCCCAATGTGTCTGTAATGCAATGTCACTGTGCTG 717
QY      578 AGCTGTGACCTTATGACCTCATAGAGATGCCCTCTGAAAGCCAACTCATGACAGATG 637
Db      716 AGCTGTGACCTTATGACCTCATAGAGATGCCCTCTGAAAGCCAACTCATGACAGATG 657
QY      638 ACCTCCCTGCACTTCACTTCTGCTTTGGGGCAGGCTTGTGCACTGCTGATGCT 697
Db      656 ACCTCCCTGCACTTCACTTCTGCTTTGGGGCAGGCTTGTGCACTGCTGATGCT 597
QY      698 CCGCTTGAAGCTGTGTCAAGACGAGATATGATGAACTGCTGCGGCAATGAGTACG 757
Db      596 CCGCTTGAAGCTGTGTCAAGACGAGATATGATGAACTGCTGCGGCAATGAGTACG 537
QY      758 CTGGCACTGTGCTTACCTATGCTCAGAGAGAGGAGCCCGAGCTTCTCAAAAGGT 817
Db      536 CTGGCACTGTGCTTACCTATGCTCAGAGAGAGGAGCCCGAGCTTCTCAAAAGGT 477
QY      818 TCATGCTCTCTTCTTCTGCTTGGGTTCCTGGAAGCTGTGATGTTCTGCACTTATGAGC 877
Db      476 TCATGCTCTCTTCTTCTGCTTGGGTTCCTGGAAGCTGTGATGTTCTGCACTTATGAGC 417
QY      878 AGCTGAACGAGCCCTCATGCTGCTGCACTTCCGAGAGAGGCTCCCTTCTGA 930
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RESULT 11
B1692548      938 bp      mRNA      linear      EST 18-SEP-2001
LOCUS      60334309.F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5370646 5'
DEFINITION      B1692548
VERSION      B1692548.1 GI:15655177
KEYWORDS      EST.
ACCESSION      B1692548
VERSION      B1692548.1 GI:15655177
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Tissue: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 938)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgsbds-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11943 row: f column: 23
High quality sequence stop: 812.

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FEATURES
Source      1..938
            /organism="Mus musculus"
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/clone="IMAGE:5370646"
/tissue_type="tumor, biopsy sample"
/dev stage="5 months"
/lab_host="MDH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1: Salt;
Site: 2: NCI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT      173 a      302 c      254 g      209 t
ORIGIN

```

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Query Match      70.2%; Score 652.4; DB 12; Length 938;
Best Local Similarity 88.1%; Pred. No. 2.5e-156;
Matches 721; Conservative 0; Mismatches 96; Indels 1; Gaps 1;

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QY      109 GCTAAAGTCCGGTTACAGATCCAGAGAAAGTCAGGAGGCGCGCTACAGCCAGC 168
Db      2 GCTAAAGTCCGGTTACAGATCCAGAGAAAGTCAGGAGGCGCGCTACAGCCAGC 61
QY      169 GCCCAGTACCGCGGTGTATGAGCACTTTGACATGTGTGCTACTGAGGCGCCCGA 228
Db      62 GCCCAGTACCGCGGTGTATGAGCACTTTGACATGTGTGCTACTGAGGCGCGCA 121
QY      229 AGCTCTCAATGAGGCTGAGTGGCGGCTGAGAGGCCAAATGAGCTTGCCTGTGCGC 288
Db      122 AGCTCTCAATGAGGCTGAGTGGCGGCTGAGAGGCCAAATGAGCTTGCCTGTGCGC 181
QY      289 ATCGGCTGTATGATTTCTGTCAAAAGTTCTTACACAAAGGCTTGTGACATGCCAGATT 348
Db      182 ATCGGCTGTATGATTTCTGTCAAAAGTTCTTACACAAAGGCTTGTGACATGCCAGATT 241
QY      349 GGGAGCGCGCTCTGAGAGGAGACACACAGAGTGCCTGAGTGTGAGTGGCCCAACC 408
Db      242 GGGAGCGCGCTCTGAGAGTGTGACACACAGAGTGCCTGAGTGTGAGTGGCCCAACC 301
QY      409 ACGGATGTGTAAAGTCCGATTCGATTCAGAGCTGAGCGCGGCTGAGAGTGTGAGATAC 468
Db      302 ACGGATGTGTAAAGTCCGATTCGATTCAGAGCTGAGCGCGGCTGAGAGTGTGAGATAC 361
QY      469 CAAAGACCGCTCAATGCTCTACAGACCAATGCCGAGAGGAGGTTCCGGGAGCTCTGG 528
Db      362 CAAAGACCGCTCAATGCTCTACAGACCAATGCCGAGAGGAGGTTCCGGGAGCTCTGG 421
QY      529 AAAGGACCTCTCCCAATGTTGCTGTATGCAATTGTCAACTGTGTGAGCTGTGAC 588
Db      422 AAAGGACCTCTCCCAATGTTGCTGTATGCAATTGTCAACTGTGTGAGCTGTGAC 481
QY      589 TATGACCTCATAGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTGCTGC 648
Db      482 TATGACCTCATAGATGCTCTCTGAAAGCCAACTCATGACAGATGACCTGCTGC 541
QY      649 CACTTCACTTGCCTTGGGAGAGGCTTGTGACCACTGTGATGCTGCTGCTGTGAGC 708
Db      542 CACTTCACTTGCCTTGGGAGAGGCTTGTGACCACTGTGATGCTGCTGCTGTGAGC 601
QY      709 GTGTGAAAGACAGATATCATGAATCTGCTGCGGCTGAGTACAGAGGCTGAGCACTG 768
Db      602 GTGTGAAAGACAGATATCATGAATCTGCTGCGGCTGAGTACAGAGGCTGAGCACTG 661
QY      769 GCCCTTACCATGCTCCAGAGAGGAGGAGGAGGCTTCTCAAAAGGTTTATGCTGCTCC 828
Db      662 GCCCTTACCATGCTCCAGAGAGGAGGAGGAGGCTTCTCAAAAGGTTTATGCTGCTCC 721
QY      829 TTTCCTGCTGTTGGTCTCTGGAAGCTGTGATGTTCTGACCTATGAGCACTGAAGCA 888
Db      722 TTTCCTGCTGTTGGTCTCTGGAAGCTGTGATGTTCTGACCTATGAGCACTGAAGCA 780
QY      889 GCCCTATGAGCTCTGCACTTCCGAGAGGCTGCTT 926
Db      781 CCTTATGAGCTCTGCACTTCCGAGAGGCTGCTT 818

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RESULT 12
AL575087/c 1125 bp mRNA linear EST 01-JUN-2003
LOCUS
DEFINITION AL575087 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD1063YE20 3-PRIME, mRNA sequence.
ACCESSION AL575087
VERSION AL575087.2 GI:31333395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1125)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12935911.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5666.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1063BC10NPLcluster=5666.r Contact :
Peng Liang Email : filiang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1063BC10NPL.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSOD1063YE20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 264 a 252 c 349 g 207 t 53 others
ORIGIN
Query Match 69.6%; Score 647.6; DB 9; Length 1125;
Best Local Similarity 93.3%; Pred. No. 4,8e-155;
Matches 667; Conservative 25; Mismatches 20; Indels 3; Gaps 2;
QY 219 GGGCCCCGAAAGCCTCTCAATGGGCTGTGTCGGCGCTGAGGCGCAATGAGCTTGC 278
DB 1028 GGGSCCCCGAAGCTTATGAGGCTGTGTCGGCGCTGAGGCGCAATGAGCTTGC 969
QY 279 CTCTGCGCATCGGCTGTATGATTTGTCAACAGTTCTACACCAAGGGCTGTAGCA 338
DB 968 YCTCTCCGCAATCGCTGTATGATTTKTAACATTTTAMMCAAGGCTGTAGCA 909
QY 339 TCCAGCATTTGGAGAGCGCTCTCTAGCAGGAGCAACAAGGTCCTGTGTGCTGT 388
DB 908 TCCAGCATTTGGAGAGCGCTCTCTCTAGCAGGAGCAACAAGGTCCTGTGTGCTGT 849
QY 399 GGGCCAGCCAGCATGAGTGTAAAGTCCGATTCAGCTCAGGCGCGGCTGAGAGTGG 458
DB 848 GGGCCAGCCAGCATGAGTGTAAAGTCCGATTCAGCTCAGGCGCGGCTGAGAGTGG 789
QY 459 TCGAGATACCAAGACCGTCAATGCTTACAGACATTGCCGAGAGAGAGGTTCCG 518
DB 788 TCGAGATACCAAGACCGTCAATGCTTACAGACATTGCCGAGAGAGAGGTTCCG 729
QY 519 GGGCTCTGAGAGAGGAGCTCTCCCAATGTTCTGTATGCGCATTTGCAACATGCTGA 578
DB 728 GGGCTCTGAGAGAGGAGCTCTCCCAATGTTCTGTATGCGCATTTGCAACATGCTGA 669
QY 579 GGTGTGACTATGACTCATCAGATGAGTCCCTCTGAAAGCAACTCATGACAGATGA 638

RESULT 13
BP976529 859 bp mRNA linear EST 22-JAN-2001
LOCUS
DEFINITION 602244382.F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:433533 5',
mRNA sequence.
ACCESSION BP976529
VERSION BP976529.1 GI:12343744
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LCM1206 row: d column: 22
High quality sequence stop: 807.
Location/Qualifiers
1..859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:433533"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 144 a 276 c 223 g 216 t
ORIGIN
Query Match 68.9%; Score 640.6; DB 10; Length 859;

Fri Feb 6 16:59:29 2004

us-09-884-814-2.rst

Page 13

QY	762	CCACCTGTGCGCTTACCATGTCTCCAGAGGAGGGGGCCCCGAGCTTTCACAAAGGGTTCAT	821
Db	601	TCACTGTGTGCCCTTACATGCTCTCCGAGAGGAGGAGCCCCGCGCTTTCACAAAGGGTTCAT	660
QY	822	GCCCTCCTTCTCCGCGTGGGTTCCTGGAGCCTGTGTATGTTCCTCACTTATGACAGCT	881
Db	661	GCGTTCCTTCTTCGCTTGGGATCTTGGAAGCTAGTATGTT-GTACCTTATAGGACGCT	719
QY	882	GAACGAGCCCTCATGGCTGCTGCACCTTCCCGAGAGGCTCCCTTCTGA	930
Db	720	CAAAAGGCTTAATGGGCTGCCACCAACTCTGGAGAGGACCTTTCTGA	768

RESULT 15	AL525249	1201 bp	RNA	EST 22-MAY-2003
LOCUS	AL525249			
DEFINITION	AL525249 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens			
ACCESSION	AL525249			
VERSION	AL525249.2	GI:31043504		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	Li, W. B., Gruber, C., Jesssee, J., and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12788742.			

Genoscope - Centre National de Sequenage
BP 101 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5666.r For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC01A1FI10P&cluster=5666.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC01A1FI10P&cluster=5666.r). Contact
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/>, Invitrogen Corporation 1600
Faraday Avenue Genom/sequence ID : CS0DC01A1FI10P.
Location/Qualifiers
1..1201

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC011YK21"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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/clone_1ist_strand_cdna was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      261 a      316 c      313 g      273 t      38 others
ORIGIN

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Query Match	68.2%;	Score 634.6;	DB 9;	Length 1201;
Best Local Similarity	92.4%;	Pred. No. 1.1e-15;		
Matches 666;	Conservative 41;	Mismatches 11;	Indels 3;	Gaps 1;

QY 1 ATGTTGGGTTCAAGGCGACAGATGAGCCCTTACGTGCACATGTAAATTTCTTGGAGCT 60
Db 364 ATGTTGGGTTCAAGGCGACAGATGAGCCCTTACGTGCACATGTAAATTTCTTGGAGCT 423
QY 61 GGCACAGTGCCTGATTCGAGATTCATCATCTTCTCTGATATAGCTAAAGTCCG 120
Db 424 GGCACAGTGCCTGATTCGAGATTCATCATCTTCTCTGATATAGCTAAAGTCCG 483
QY 121 TTACGATCCAGAGAAAGTCAAGGGCCAGTGGCGGTACAGCCAGGCCCCAATACCG 180
Db 484 TTACGATCCAGAGAAAGTCAAGGGCCAGTGGCGGTACAGCTACAGGCCCATACCG 543

[illegible]

Search completed: February 4, 2004, 20:08:11
Job time : 2418 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd

OM protein - protein search, using sw model

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Run on:      February 4, 2004, 09:15:38 ; Search time 42 Seconds
              (without alignments)
              1167.774 Million cell updates/second
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Title: US-09-884-814-1

Sequence: 1 MVGFKATDVPTATVKFLGA.....TYEQLKRALMAACTSREAPF 309

Scoring table: BLOSUM62, Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

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Total number of hits satisfying chosen parameters: 1107863
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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A_Geneseq_19J001: *

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3: /SIDS1/gcgatga/genseeq/genseqp-emb1/AA1982.DAT *

4: /SIDS1/gcgatga/genseeq/genseqp-emb1/AA1983.DAT *

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6: /SIDS1/gcgatga/genseeq/genseqp-emb1/AA1985.DAT *

7: /SIDS1/gcgatga/genseeq/genseqp-emb1/AA1986.DAT *

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24: /SIDS1/gcgatga/genseeq/genseqp-emb1/AA2003.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1576	100.0	309	20	AAI31803	Human uncoupling p
2	1576	100.0	309	20	AAI28751	UCP2 amino acid se
3	1576	100.0	309	21	AAI45002	Trilalrik human un
4	1576	100.0	309	21	AAI44592	Human uncoupling p
5	1576	100.0	309	22	AAU72342	Human uncoupling p
6	1576	100.0	314	22	AAU09077	Human uncoupling p
7	1572	99.7	309	19	AAW24000	Complete chimeric
8	1572	99.7	309	19	AAI28853	UCP2 amino acid se
9	1572	99.7	309	20	AAW89546	Full length human

10	1572	99.7	309	21	AAAB7018	Protein associated
11	1572	99.7	309	21	AAAY7998	Human uncoupling p
12	1572	99.7	309	21	AAAY4232	Human mitochondria
13	1570	99.6	309	19	AAAG9166	Human respiration
14	1570	99.6	309	20	AAAY28332	UCP2 amino acid se
15	1570	99.6	309	23	AAU98901	Human uncoupling p
16	1565	99.3	309	20	AAAB5669	Human UCP-2 (uncou
17	1551	98.4	309	17	AAAB1282	Body weight disordr
18	1530	96.4	295	19	AAAB3998	Partial human C5 g
19	1459	95.1	299	17	AAAB1281	Human body weight
20	1282	81.3	303	19	AAAB23997	Mouse C5 gene prod
21	1282	81.3	303	21	AAAY7997	Mouse uncoupling p
22	1279	81.2	303	20	AAAB69545	Full length mouse
23	1279	81.2	303	21	AAAB27017	Protein associated
24	1273	80.8	303	21	AAAB91280	Brown fat uncouplil
25	1181.5	75.0	397	15	AAAB1596	Protein encoded by
26	1180.5	74.9	308	19	AAAB81595	Mouse uncoupling F
27	1180.5	74.9	308	20	AAAB88280	Mouse uncoupling F
28	1178.5	74.8	308	20	AAAY29833	Mouse uncoupling F
29	1178.5	74.8	308	21	AAAB85116	A murine uncouplir
30	1178.5	74.8	308	21	AAAY74452	Murine mitochondri
31	1178.5	74.8	308	22	AAAB04722	Mouse uncoupling F
32	1162.5	73.8	432	20	AAAY2835	Mouse uncoupling F
33	1162.5	73.8	432	20	AAAB85117	A murine uncouplir
34	1162.5	73.8	432	21	AAAY74453	Murine mitochondri
35	1162.5	73.8	432	21	AAAE04730	Mouse uncoupling F
36	1149.5	72.9	312	19	AAAB63197	Human uncoupling F
37	1149.5	72.9	312	19	AAAB68137	Human uncoupling F
38	1149.5	72.9	312	20	AAAY31904	Human uncoupling F
39	1149.5	72.9	312	20	AAAB8667	Human uncoupling F
40	1149.5	72.9	312	20	AAAB88279	Human uncoupling F
41	1149.5	72.9	312	21	AAAY54600	Amino acid sequenc
42	1149.5	72.9	312	21	AAAY44253	Human mitochondria
43	1149.5	72.9	312	22	AAAB04258	Human uncoupling F
44	1149.5	72.9	312	22	AAAB68050	Amino acid sequenc
45	1149.5	72.9	312	22	AAAB74296	Human UCP3 protei

ALIGNMENTS

RESULT 1
AAV31903
ID AAV31903 standard; Protein; 309 AA.

XX
DT 21-DEC-1999 (first entry)

Human uncoupling protein 2.

AA Uncoupling protein 2; UCP2; human; obesity; diabetes; diagnosis;
KM gene therapy.
KW

OS Homo sapiens

Key	Location/Qualifiers
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PN WO9948905-A1

30-SEP-1999. PD

PF 23-MAR-1999; 99WO-US06317.
YY

PR 23-MAR-1998; 98US-00189/2.

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PF 29-JUL-1999; 99WO-US17246.
 XX 29-JUL-1998; 98US-0124293.
 PR (TULA-) TULARIK INC.
 XX Chen J, Amaral MC;
 PI WPI; 2000-195157/17.
 DR N-PSDB; AAZ50624.
 XX Novel recombinant nucleic acids encoding uncoupling protein-2 with
 PT specific alanine and threonine residues, useful for treating body
 PT weight disorders e.g. obesity -
 PS Claim 2; Page 40; 40pp; English.
 XX The present sequence is a novel human uncoupling protein-2 (UCP2) used
 CC for treatment of body weight disorders. This is expressed in a wide
 CC range of tissues ranging from the brain to muscle and fat cells. UCP2 is
 CC used as a therapeutic to treat obese animals by increasing the rate of
 CC fat metabolism. The protein is also used in screening assays to identify
 CC modulators of UCP2 biological activity, or as pharmaceutical agents to
 CC treat disorders, like obesity and underweight disorders.
 CC
 XX Sequence 309 AA;
 SQ
 Query Match 100.0%; Score 1576; DB 21; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-158;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGFKADVPEPTATVVKFLGAGTAACIADLITFPDIAKRVRLQIQESQGPVATASQYR 60
 DB 1 MVGFKADVPEPTATVVKFLGAGTAACIADLITFPDIAKRVRLQIQESQGPVATASQYR 60
 QY 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVKQYTKGSEHASTGRL 120
 DB 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVKQYTKGSEHASTGRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 QY 181 PNVARNAIIVNCAELVYDILIKDALLKANLMTDDLPCHFTSAFAGCCTVIASPVVYKT 240
 DB 181 PNVARNAIIVNCAELVYDILIKDALLKANLMTDDLPCHFTSAFAGCCTVIASPVVYKT 240
 QY 241 RYMNSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFLRLGSMNVMMFTVYEQLRALMA 300
 DB 241 RYMNSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFLRLGSMNVMMFTVYEQLRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 RESULT 4
 ID AAY44292 standard; Protein; 309 AA.
 XX AAY44292;
 AC AAY44292;
 XX 29-FEB-2000 (first entry)
 DT 29-FEB-2000 (first entry)
 XX Human uncoupling protein-2.
 DE Human uncoupling protein-2.
 XX Human uncoupling protein-2; UCP; immune response; electron transport;
 KM oxidative phosphorylation; Major histocompatibility complex;
 KM MHC class II HLA-DR; proton motor force; mitochondrial membrane potential;
 KM mitochondrial metabolism; cancer; autoimmune disease;
 KM neurodegenerative disorder.
 XX Homo sapiens.
 OS

XX WO9933953-A2.
 PN 28-OCT-1999.
 XX 30-MAR-1999; 99WO-US06874.
 PF 17-APR-1998; 98US-0082250.
 PR 29-JUL-1998; 98US-0094519.
 PR 24-SEP-1998; 98US-0101580.
 XX (UYVE-) UNIV VERMONT.
 PA Newell MK;
 XX WPI; 2000-096773/08.
 DR N-PSDB; AAZ29323.
 XX Use of cell surface and membrane characteristics for developing
 PT products for treating cancers, autoimmune diseases or neurodegenerative
 PT diseases -
 PS Disclosure; Page 118-119; 123pp; English.
 XX The present sequence is human uncoupling protein-2. UCPS can cause
 CC the reversible uncoupling of electron transport and oxidative
 CC phosphorylation, which leads to a decrease in the mitochondrial membrane
 CC potential. This can induce lysis in a tumour cell by inducing the
 CC expression of MHC class II HLA-DR. These methods can be used for
 CC regulating cell growth and division to control disease processes by
 CC manipulating mitochondrial metabolism and the expression of cell surface
 CC immune proteins. They can be used for treating diseases associated with
 CC excessive cellular division, aberrant differentiation, and premature
 CC cellular death, e.g. cancers, autoimmune diseases, neurodegenerative
 CC disorders etc.
 CC
 XX Sequence 309 AA;
 SQ
 Query Match 100.0%; Score 1576; DB 21; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-158;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGFKADVPEPTATVVKFLGAGTAACIADLITFPDIAKRVRLQIQESQGPVATASQYR 60
 DB 1 MVGFKADVPEPTATVVKFLGAGTAACIADLITFPDIAKRVRLQIQESQGPVATASQYR 60
 QY 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVKQYTKGSEHASTGRL 120
 DB 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVKQYTKGSEHASTGRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAOARAGGRRYOSTVNAKTIAREEGFRGLMKGTS 180
 QY 181 PNVARNAIIVNCAELVYDILIKDALLKANLMTDDLPCHFTSAFAGCCTVIASPVVYKT 240
 DB 181 PNVARNAIIVNCAELVYDILIKDALLKANLMTDDLPCHFTSAFAGCCTVIASPVVYKT 240
 QY 241 RYMNSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFLRLGSMNVMMFTVYEQLRALMA 300
 DB 241 RYMNSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFLRLGSMNVMMFTVYEQLRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 RESULT 5
 ID AAY72342 standard; Protein; 309 AA.
 XX AAY72342;
 AC AAY72342;
 XX AAY72342;
 XX

DT 24-APR-2001 (first entry)
 XX Human uncoupling protein, UCP-2.
 DE
 XX Human; uncoupling protein; UCP-2; cancer; brain; renal; antiviral;
 KM antibacterial; antifungal; cytostatic; immunosuppressive; scleroderma;
 KM antiarthritic; dermatological; UCP inhibitor; therapy; antithematic;
 KM rheumatoid arthritis; leukaemia; tumour; autoimmune disease; SLE;
 KM systemic lupus erythematosus; celiac disease; infectious disease;
 KM pemphigus vulgaris.
 XX
 OS Homo sapiens.
 XX WO200078941-A2.
 PN
 XX 28-DEC-2000.
 PD
 XX 22-JUN-2000; 2000WC-US17245.
 PF
 XX 23-JUN-1999; 99US-0140574.
 PR
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PA
 XX Newell MK;
 FI
 XX WPI; 2001-102716/11.
 DR N-PSDB; AAD02388.
 DR
 XX Inhibiting plasma membrane uncoupling protein expression in tumor cells
 PT and rapidly dividing bacterial cells, for treating cancer and
 PT infectious diseases -
 PT
 XX Disclosure; Page 104-105; 106pp; English.
 PS
 XX The present sequence is human uncoupling protein, UCP-2. The
 CC present invention relates to a method for inhibiting the expression
 CC of plasma membrane uncoupling protein (UCP) in a cell by a plasma
 CC membrane UCP inhibitor. UCP is expressed on lysosomal membranes
 CC and plasma membranes of rapidly dividing cells, but absent in growth
 CC arrested or chemotherapy resistant cells. This method is useful in the
 CC inhibition of plasma membrane UCP expression in tumor cells,
 CC lymphocytes, pancreatic beta cells, rapidly dividing bacterial cells
 CC or B cells. UCP inhibitor is useful in the prevention and treatment of
 CC infectious disease, rheumatoid arthritis, scleroderma and cancers such
 CC as brain cancer, leukemia, renal cancer, and tumours. The UCP activator
 CC is useful in the treatment of autoimmune diseases such as systemic
 CC lupus erythematosus (SLE), celiac disease and pemphigus vulgaris. UCP
 CC is also useful for inducing cellular division in nerve cells.
 CC
 XX Sequence 309 AA;
 SQ
 Query Match 100.0%; Score 1576; DB 22; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-158; Indels 0; Gaps 0;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGFKATDVPPTATVTKFLGAGTAACTADLTTPDTAKVRLQIQESGQPVATASQYR 60
 DB 1 MVGFKATDVPPTATVTKFLGAGTAACTADLTTPDTAKVRLQIQESGQPVATASQYR 60
 QY 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLYDVSKQFYTKGSHASIGSRL 120
 DB 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLYDVSKQFYTKGSHASIGSRL 120
 QY 121 LAGSTTGALAAVAAPFDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREEGFGGLMKGTS 180
 DB 121 LAGSTTGALAAVAAPFDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREEGFGGLMKGTS 180
 QY 121 LAGSTTGALAAVAAPFDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREEGFGGLMKGTS 180
 DB 121 LAGSTTGALAAVAAPFDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREEGFGGLMKGTS 180
 QY 181 PVNARNALVNCHEITVYLLIDALLKAVLMTDDI.PCHFTSAFGAGFCTTYIASPVVVKI 240
 DB 181 PVNARNALVNCHEITVYLLIDALLKAVLMTDDI.PCHFTSAFGAGFCTTYIASPVVVKI 240
 QY 241 RYMNSALGOYSSAGHCALTMLQKSGPRAFYKGFPSPFLIGSNVNVFVTTYEQKRALMA 300
 DB 241 RYMNSALGOYSSAGHCALTMLQKSGPRAFYKGFPSPFLIGSNVNVFVTTYEQKRALMA 300

DB 241 RYMNSALGOYSSAGHCALTMLQKSGPRAFYKGFPSPFLIGSNVNVFVTTYEQKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 RESULT 6
 AAU09077
 ID AAU09077 standard; Protein; 314 AA.
 XX
 AC AAU09077;
 XX
 DT 13-DEC-2001 (first entry)
 DE
 XX Human uncoupling protein, UCP-2.
 XX
 KM Human; uncoupling protein; UCP-2; transgenic plant; fuel metabolism;
 KM antibacterial; bacterial infection; environmental stress; food.
 XX
 OS Homo sapiens.
 XX WO200175131-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WC-US10236.
 PF
 XX 31-MAR-2000; 2000US-193533P.
 PR
 XX (UYTE-) UNIV TECHNOLOGY CORP.
 PA
 XX Berry-Lowe SL, Newell MK;
 FI
 XX WPI; 2001-626442/72.
 DR N-PSDB; AAS14819.
 DR
 XX Plants expressing heterologous cell-wall uncoupling protein, have
 PT altered metabolism, resistance to infection and stress sensitivity -
 PT
 XX Disclosure; Page 59-60; 72pp; English.
 PS
 XX The invention relates to a transgenic plant expressing a cell-wall UCP
 CC (uncoupling protein) encoded by a heterologous gene. The
 CC heterologous UCP, when expressed in the plant cell wall, plasma
 CC membrane or chloroplast regulates the fuel metabolism of the plant.
 CC Regulating expression or activity of UCP is used to control fuel
 CC metabolism, especially reducing UCP expression produces nutritionally
 CC improved plants and protects against infection e.g. bacterial, while
 CC decreasing expression improves sensitivity to light and cold. Altering
 CC UCP activity can improve crop productivity and durability towards
 CC environmental stress, and it eliminates time-consuming and expensive
 CC maintenance and repeated application of chemicals. The present
 CC sequence represents human UCP-2 and is used as the heterologous UCP in
 CC the method of the invention.
 CC
 XX Sequence 314 AA;
 SQ
 Query Match 100.0%; Score 1576; DB 22; Length 314;
 Best Local Similarity 100.0%; Pred. No. 3.2e-158; Indels 0; Gaps 0;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGFKATDVPPTATVTKFLGAGTAACTADLTTPDTAKVRLQIQESGQPVATASQYR 60
 DB 6 MVGFKATDVPPTATVTKFLGAGTAACTADLTTPDTAKVRLQIQESGQPVATASQYR 65
 QY 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLYDVSKQFYTKGSHASIGSRL 120
 DB 66 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLYDVSKQFYTKGSHASIGSRL 125
 QY 121 LAGSTTGALAAVAAPFDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREEGFGGLMKGTS 180
 DB 126 LAGSTTGALAAVAAPFDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREEGFGGLMKGTS 185

QY 181 PNVARNAIYVCAELVYTDLIKALLKANIMTDDJPCHTFSAFAGFCTTVIASPVVYKT 240
 DB 186 PNVARNAIYVCAELVYTDLIKALLKANIMTDDJPCHTFSAFAGFCTTVIASPVVYKT 245
 QY 241 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
 DB 246 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 305
 QY 301 ACTSREAPF 309
 DB 306 ACTSREAPF 314

RESULT 7
 AAM24000
 ID AAM24000 standard; Protein; 309 AA.

AC AAM24000;
 DT 28-MAY-1998 (first entry)
 DE Complete chimeric mouse/human C5 gene product.
 KW Human; mouse; C5 gene; weight disorder; obesity; chimeric.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 XX US5702902-A.
 XX 30-DEC-1997.
 XX 23-AUG-1995; 95US-0518878.
 XX 23-AUG-1995; 95US-0518878.
 XX 23-AUG-1995; 95US-0518878.
 XX 23-AUG-1994; 94US-0294522.
 XX 06-JUN-1995; 95US-0470868.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Targadia LA;
 DR WPI; 1998-076410/07.
 XX

PT Diagnosis of body weight disorders - by detecting abnormal C5 gene expression
 PS Claim 1; Column 87-88; 71pp; English.
 CC This is the amino acid sequence for the chimeric murine/human C5 protein. The C5 gene shows differential expression in body weight disorder states relative to expression in a normal body. Body weight disorders can be diagnosed using tests comprising the detection of abnormal levels of the C5 gene transcript (or the encoded protein). The method can be used to diagnose, e.g. obesity.
 CC

SC Sequence 309 AA;
 Query Match 99.7%; Score 1572; DB 19; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVSFKATDVPEPTATVVFELGAGTACTADITPPLDTAKVRLIOGESGQPVRAVTAQYR 60
 DB 1 MVSFKATDVPEPTATVVFELGAGTACTADITPPLDTAKVRLIOGESGQPVRAVTAQYR 60
 QY 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASISGRL 120
 DB 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASISGRL 120
 QY 121 LAGSTGALAAVAAQPTDVVKVRFQQAARAGGRRYQSTVNAKYTIAEEGFRGLMKGTS 180
 DB 121 LAGSTGALAAVAAQPTDVVKVRFQQAARAGGRRYQSTVNAKYTIAEEGFRGLMKGTS 180

DB 121 LAGSTGALAAVAAQPTDVVKVRFQQAARAGGRRYQSTVNAKYTIAEEGFRGLMKGTS 180
 QY 181 PNVARNAIYVCAELVYTDLIKALLKANIMTDDJPCHTFSAFAGFCTTVIASPVVYKT 240
 DB 186 PNVARNAIYVCAELVYTDLIKALLKANIMTDDJPCHTFSAFAGFCTTVIASPVVYKT 245
 QY 241 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
 DB 246 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 305
 QY 301 ACTSREAPF 309
 DB 306 ACTSREAPF 314

RESULT 8
 AAY28353
 ID AAY28353 standard; Protein; 309 AA.

AC AAY28353;
 DT 19-OCT-1999 (first entry)
 DE UCP2 amino acid sequence (Gimeno variant).
 KW uncoupling protein; amino acid; mitochondria; diabetes;
 KW brown adipose tissue; wild type; obesity; thermo-regulation.
 OS Homo sapiens.
 XX WO9937812-A1.
 XX 29-JUL-1999.
 XX 21-JAN-1999; 99WO-US01198.
 XX 23-JAN-1998; 98US-0012218.
 XX (ORCH-) ORCHID BIOCOMPUTER INC.
 XX Vrolijk LP;
 DR WPI; 1999-468144/39.
 DR N-PEDB; AAX99436.
 XX

PT A novel single nucleotide polymorphism of the uncoupling protein 2 gene, useful for diagnosis, prognosis and treatment of obesity
 PS Disclosure; Fig 1; 68pp; English.
 CC This is the amino acid sequence of uncoupling protein-2 (UCP-2) as reported by Gimeno et al, 1997 (direct submission).
 CC Identifying a UCP2 polymorphism, especially Val55 (thymine at nucleotide 164), can be used to diagnose obesity, non-insulin dependent diabetes mellitus and other UCP2 related diseases (claimed). Wild-type UCP2 generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2 related diseases include atherosclerosis, hyperinsulinemia, chronic inflammation, thermogenesis, apoptosis and cachexia.
 CC

SC Sequence 309 AA;
 Query Match 99.7%; Score 1572; DB 20; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVSFKATDVPEPTATVVFELGAGTACTADITPPLDTAKVRLIOGESGQPVRAVTAQYR 60
 DB 1 MVSFKATDVPEPTATVVFELGAGTACTADITPPLDTAKVRLIOGESGQPVRAVTAQYR 60
 QY 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASISGRL 120
 DB 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASISGRL 120

QY 121 LAGSTGALA VAAV AQP TDVVKR FQAQARAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 DB 121 LAGSTGALA VAAV AQP TDVVKR FQAQARAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 QY 181 PNVARNAI VNCALVTYDLIKDALKANIMTDLPCHFTSAFGAGFTTVIASPDVVKTI 240
 DB 181 PNVARNAI VNCALVTYDLIKDALKANIMTDLPCHFTSAFGAGFTTVIASPDVVKTI 240
 QY 241 RYMSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 RESULT 9
 ID AAM89546 standard; Protein; 309 AA.
 AC AAM89546;
 XX 31-MAR-1999 (first entry)
 DT 31-MAR-1999 (first entry)
 DE Full length human C5 protein sequence.
 XX Body weight disorder; obesity; appetite regulation; thermoregulation;
 KW anorexia; abnormal food intake; cachexia; thermogenesis.
 OS Homo sapiens.
 PN US5853975-A.
 XX 29-DEC-1998.
 PD 29-DEC-1998.
 PF 26-FEB-1997; 97US-0807861.
 XX 26-FEB-1997; 97US-0807861.
 PR 23-AUG-1994; 94US-0294522.
 PR 06-JUN-1995; 95US-0470868.
 PR 23-AUG-1995; 95US-0518878.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Tartaglia LA;
 PI WPI: 1999-054892/08.
 DR N-PsDB; AAV82381.
 XX Identifying modulators of C5 protein uncoupling activity - used as
 PT potential regulators of thermogenesis, appetite and body weight,
 PR e.g. for treating obesity, anorexia and cachexia
 XX Claim 7; Fig 16; 83pp; English.
 PS The present invention describes a method for identifying a compound (I)
 CC that modulates C5 protein uncoupling activity by: (a) treating a test
 CC compound with C5 or cells expressing it; (b) measuring the level of
 CC uncoupling activity; and (c) comparing this with level of activity in
 CC the absence of the test compound. Any difference in the levels indicates
 CC a modulator. C5 protein has uncoupling activity, i.e. it can transport
 CC protons across the mitochondrial inner membrane, reducing the proton
 CC motive force and allowing dissipation of caloric energy as heat. It is
 CC thus a regulator of thermogenesis and is involved in body weight
 CC regulation. (I) are potentially useful in treatment of body weight
 CC disorders, regulation of appetite and thermoregulation, e.g. in cases of
 CC obesity, anorexia, abnormal food intake and cachexia. The present
 CC sequence represents the full length human C5 protein sequence, from
 CC the present invention.
 XX Sequence 309 AA;
 SQ

Query Match 99.7%; Score 1572; DB 20; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MVSFKATDVPPNATVYVFIAGAFACIADLITPELDTAKVRLQIGESGQPYRATASQYR 60
 DB 1 MVSFKATDVPPNATVYVFIAGAFACIADLITPELDTAKVRLQIGESGQPYRATASQYR 60
 QY 61 GWNGITLITWREGPSRLYNGLVAGIQRMSPASVRIQLYDSVXQFYTKGSEHASIGSRL 120
 DB 61 GWNGITLITWREGPSRLYNGLVAGIQRMSPASVRIQLYDSVXQFYTKGSEHASIGSRL 120
 QY 121 LAGSTGALA VAAV AQP TDVVKR FQAQARAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 DB 121 LAGSTGALA VAAV AQP TDVVKR FQAQARAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 QY 181 PNVARNAI VNCALVTYDLIKDALKANIMTDLPCHFTSAFGAGFTTVIASPDVVKTI 240
 DB 181 PNVARNAI VNCALVTYDLIKDALKANIMTDLPCHFTSAFGAGFTTVIASPDVVKTI 240
 QY 241 RYMSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 RESULT 10
 ID AAB27018 standard; Protein; 309 AA.
 AC AAB27018;
 XX 06-FEB-2001 (first entry)
 DT 06-FEB-2001 (first entry)
 DE Protein associated with body weight disorders, SEQ ID NO: 51.
 XX Mouse; body weight; immunomodulator; anorectic; obesity; cachexia;
 KW thermogenesis; appetite.
 OS Mus sp.
 PN US6121017-A.
 XX 19-SEP-2000.
 PD 19-SEP-2000.
 PF 08-OCT-1997; 97US-0946719.
 XX 26-FEB-1997; 97US-0807861.
 PR 23-AUG-1994; 94US-0294522.
 PR 06-JUN-1995; 95US-0470868.
 PR 23-AUG-1995; 95US-0518878.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Tartaglia LA;
 PI WPI: 2000-618197/59.
 DR N-PsDB; AAA99716.
 XX New human C5 gene and gene product, useful in regulating mammalian body
 PT weight and modulating thermogenesis, especially useful for treating
 PT body weight disorders, e.g. obesity or cachexia
 XX Claim 1; Fig 17B; 84pp; English.
 PS The present sequence is encoded by a nucleotide sequence which was
 CC found to be differentially expressed in body weight disorder
 CC states. It may be useful in modulating processes relating to mammalian
 CC body weight regulation, including treatment of body weight disorders,
 CC e.g. obesity or cachexia, and modulation of thermogenesis. It is also

CC useful in regulating appetite and/or body weight. Furthermore, it is
 CC useful for diagnostic evaluation and prognosis of various body weight
 CC disorders, and for identifying subjects exhibiting a predisposition to
 CC such conditions.

XX Sequence 309 AA;

Query Match 99.7%; Score 1572; DB 21; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWGFKATDVPPTATVKEFLGAGTAACIADLITFPDLDTAKVRLQIQESQGVPRATASQYR 60
 DB 1 MWGFKATDVPPTATVKEFLGAGTAACIADLITFPDLDTAKVRLQIQESQGVPRATVSAQYR 60
 QY 61 GVGITLTMVTRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVGITLTMVTRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQQAAPAGGRRYOSTVNAVYKTIAEEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQQAAPAGGRRYOSTVNAVYKTIAEEGFRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVTVLLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 DB 181 PNVARNAIVNCAELVTVLLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 QY 241 RYVNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVVMFVTEQLKRALMA 300
 DB 241 RYVNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 11
 ID AAY97998 standard; Protein; 309 AA.

XX AAY97998;
 XX 18-SEP-2000 (first entry)

XX Human uncoupling protein C5, SEQ ID NO:51.
 XX Body weight disorder; obesity; cachexia; differential expression;
 KW human; C5 gene; C5 protein; UCP homologue; uncoupling protein;
 KW thermogenesis; expression modulation.

XX Homo sapiens.

OS US6057109-A.

PN 02-MAY-2000.

PF 14-DEC-1998; 98US-0210681.

PR 26-FEB-1997; 97US-0807861.

PR 08-OCT-1997; 97US-0946719.

PR 23-AUG-1994; 94US-0294522.

PR 06-JUN-1995; 95US-0470868.

PR 23-AUG-1995; 95US-0518878.

PA (MILL-) MILENNIUM PHARM INC.

PI Tartaglia LA;

DR WPI; 2000-338601/29.

DR N-PSDB; AAA52254.

XX Identifying C5 gene expression modulators useful for treating obesity
 PT and cachexia comprises comparing levels of C5 expression prior to or

PT after contacting it with test compound -
 XX Examples; Fig 18A-B; 8app; English.

XX The invention relates to a method for identifying a compound that
 CC modulates expression of the novel gene C5. The method comprises
 CC contacting a cell expressing the C5 protein with a test compound, and
 CC comparing the levels of C5 expression prior to or after exposure to the
 CC test compound. A difference in expression indicates that the test
 CC compound is a C5 gene expression modulator. The C5 protein (AAY97997,
 CC AAY97999) has sequence similarity with mammalian brown fat uncoupling
 CC proteins (UCPs). In the exemplifications of the invention, the C5
 CC protein was shown to be able to uncouple ATP synthesis from oxidative
 CC phosphorylation, allowing caloric energy to be dissipated as heat. cDNA
 CC sequences encoding C5 (AAA52253, AAA52254) were isolated in an
 CC investigation to identify genes which are differentially expressed in
 CC body weight disorders such as obesity and cachexia. A compound which
 CC modulates C5 expression is useful for modulating thermogenesis, and is
 CC therefore useful for treating body weight disorders. Increasing the level
 CC of C5 gene expression and/or gene product activity increases the rate of
 CC thermogenesis and causes a reduction in body weight, which is useful for
 CC the treatment of obesity. Decreasing the level of C5 gene expression
 CC and/or C5 gene product activity decreases the rate of thermogenesis
 CC and causes an increase in body weight, which is useful for the treatment
 CC of cachexia. The present sequence represents the human C5 protein.

XX Sequence 309 AA;

Query Match 99.7%; Score 1572; DB 21; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWGFKATDVPPTATVKEFLGAGTAACIADLITFPDLDTAKVRLQIQESQGVPRATASQYR 60
 DB 1 MWGFKATDVPPTATVKEFLGAGTAACIADLITFPDLDTAKVRLQIQESQGVPRATVSAQYR 60
 QY 61 GVGITLTMVTRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVGITLTMVTRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQQAAPAGGRRYOSTVNAVYKTIAEEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQQAAPAGGRRYOSTVNAVYKTIAEEGFRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVTVLLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 DB 181 PNVARNAIVNCAELVTVLLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 QY 241 RYVNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVVMFVTEQLKRALMA 300
 DB 241 RYVNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 12
 ID AAY44252 standard; Protein; 309 AA.

XX AAY44252;

XX 28-FEB-2000 (first entry)

DE Human mitochondrial anion carrier, uncoupling protein-2.

XX Mitochondrial uncoupling protein-2; UCP-2; mitochondrial anion carrier;

KW MAC; modulator; transport protein; fatty acid anion; mitochondria;

XX assay vesicle; metabolic disorder; diabetes; obesity; cancer; human.

XX Homo sapiens.

QY 61 GVMGTTILTMVTEGPRSLYNGLVAGLQROMSPFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTTILTMVTEGPRSLYNGLVAGLQROMSPFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAAPDTPVVKVRFQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAAPDTPVVKVRFQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 QY 181 PNVAANAIVNCAELVYTDLLIKDALLKANLMTDDLPCFFTSAPGAGFCTTVIASPVVVK 240
 DB 181 PNVAANAIVNCAELVYTDLLIKDALLKANLMTDDLPCFFTSAPGAGFCTTVIASPVVVK 240
 QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYEQLEKRALMA 300
 DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYEQLEKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 14

AAV28352
 ID AAV28352 standard; protein; 309 AA.

XX AAV28352;
 AC AAV28352;

XX 19-OCT-1999 (first entry)
 DT 19-OCT-1999 (first entry)

DE UCP2 amino acid sequence (Fleury variant).
 XX

KM uncoupling protein; amino acid; mitochondria; diabetes;
 KM brown adipose tissue; wild type; obesity; thermo-regulation.

XX

OS Homo sapiens.
 XX

PN W09937812-A1.
 XX

PD 29-JUL-1999.
 XX

PF 21-JAN-1999; 99WC-US01198.
 XX

PR 23-JAN-1998; 98US-0012218.
 XX

PA (ORCH-) ORCHID BIOCOMPUTER INC.
 XX

PI Vrolijk LP;
 XX

DR WPI: 1999-469144/39.
 DR N-PSDB; AAX99435.

XX

PT A novel single nucleotide polymorphism of the uncoupling protein 2
 PT gene, useful for diagnosis, prognosis and treatment of obesity
 XX

PS Disclosure; Fig 1; 68pp; English.
 XX

CC This is the amino acid sequence of uncoupling protein-2 (UCP-2) as
 CC reported by Fleury et al, 1997 Nature genetics.
 CC Identifying a UCP2 polymorphism, especially Val55 (thymine at
 CC nucleotide 164), can be used to diagnose obesity, non-insulin dependent
 CC diabetes mellitus and other UCP2 related diseases (claimed). Wild-type
 CC UCP2 generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2
 CC related diseases include atherosclerosis, hyperinsulinemia, chronic
 CC inflammation, thermogenesis, apoptosis and cachexia.
 CC

XX

XX

SQ Sequence 309 AA;
 Query Match 99.6%; Score 1570; DB 20; Length 309;
 Best Local Similarity 99.7%; Pred. No. 1.3e-157;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDPAKRVLOIQESQGPVRAATASAOYR 60
 |||

DB 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDPAKRVLOIQESQGPVRAATASAOYR 60
 QY 61 GVMGTTILTMVTEGPRSLYNGLVAGLQROMSPFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTTILTMVTEGPRSLYNGLVAGLQROMSPFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAAPDTPVVKVRFQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAAPDTPVVKVRFQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 QY 181 PNVAANAIVNCAELVYTDLLIKDALLKANLMTDDLPCFFTSAPGAGFCTTVIASPVVVK 240
 DB 181 PNVAANAIVNCAELVYTDLLIKDALLKANLMTDDLPCFFTSAPGAGFCTTVIASPVVVK 240
 QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYEQLEKRALMA 300
 DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYEQLEKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 15

AAU98901
 ID AAU98901 standard; Protein; 309 AA.

XX AAU98901;
 AC AAU98901;

XX 22-AUG-2002 (first entry)
 DT 22-AUG-2002 (first entry)

DE Human uncoupling protein UCP-2.
 XX

KM Human; uncoupling protein; UCP-2; stroke; ischaemia; epilepsy;
 KM neurological disorder; neuronal injury; Parkinson's disease;
 KM Huntington's disease; inherited ataxia; motor neuron disease;
 KM Alzheimer's disease; traumatic brain injury; Bradykinin;
 KM serotonin; histamine; arachidonic acid.
 KM

XX

OS Homo sapiens.
 XX

PN W0200236829-A2.
 XX

PD 10-MAY-2002.
 XX

PF 01-NOV-2001; 2001WO-US45744.
 XX

PR 01-NOV-2000; 2000US-244946P.
 XX

PA (AGYT-) AGY THERAPEUTICS INC.
 XX

PI Gonzalez-Zulueta M, Shamloo M, McFarland KC, Chin D, Wieloch T;
 PI Melcher T;
 XX

DR WPI: 2002-490012/52.
 DR N-PSDB; ABK86151.

XX

PT Diagnosing occurrence of stroke or assessing a patient's susceptibility
 PT to stroke, by detecting in a patient sample an elevated level of
 PT uncoupling proteins-2 expression -
 XX

PS Disclosure; Page 79; 80pp; English.
 XX

XX

CC The invention relates to a method of diagnosing occurrence of a stroke or
 CC assessing a patient's susceptibility to a stroke, comprising detecting in
 CC a patient sample an elevated level of uncoupling proteins (UCP)-2
 CC expression. The method is useful for diagnosing occurrence of a stroke or
 CC assessing a patient's susceptibility to a stroke, where the stroke is an
 CC ischaemic stroke. The method is useful for treating a subject having or
 CC is susceptible to a neurological disorder or a neuronal injury, where the
 CC neuronal injury is a stroke, or an ischaemic stroke. The neurological
 CC disorder is selected from Parkinson's disease, Huntington's disease,
 CC inherited ataxia, motor neuron disease, Alzheimer's disease, epilepsy,

CC and traumatic brain injury. The disorder is treated with a propylactic
CC agent which increases the permeability of the blood/brain barrier, or
CC with an anticoagulant and a secondary agent selected from bradykinin,
CC serotonin, histamine and arachidonic acid. The agent is a purified
CC UCP-2 polypeptide in combination with an anticoagulant. The method is
CC also useful for screening for an agent useful for treating a neurological
CC disorder or a neuronal injury. The present sequence represents the
CC amino acid sequence of human UCP-2.
XX

SQ Sequence 309 AA;

Query Match 99.6%; Score 1570; DB 23; Length 309;

Best Local Similarity 99.7%; Pred. No. 1.3e-157;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPPTATVVKFLGAGTAACIADLITFPDLTAKVRLIQGESQGPVATASAQYR 60
DB 1 MVGFKATDVPPPTATVVKFLGAGTAACIADLITFPDLTAKVRLIQGESQGPVATASAQYR 60
QY 61 GVMGTILTMVTRTEGPRSLYNGLYAGLCROMSFASVRLGLYDSVKQFTKGEHASTGSR 120
DB 61 GVMGTILTMVTRTEGPRSLYNGLYAGLCROMSFASVRLGLYDSVKQFTKGEHASTGSR 120
QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREGFRGLWKGT 180
DB 121 LAGSTTGALAAVAVAQPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREGFRGLWKGT 180
QY 181 PVARNAALVNCALVLTLDLIKDALIKALMTDDLPCHTSAFGAGPCTTVIASPVDVKT 240
DB 181 PVARNAALVNCALVLTLDLIKDALIKALMTDDLPCHTSAFGAGPCTTVIASPVDVKT 240
QY 241 RYMNSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSEFLIGSMNVVMFVTEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSEFLIGSMNVVMFVTEQIKRALMA 300
QY 301 ACTSRAPF 309
DB 301 ACTSRAPF 309

Search completed: February 4, 2004, 09:17:59
Job time : 43 secs

Fri Feb 6 16:59:26 2004

US-09-884-814-1.rat

Page 1

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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:17:09 ; Search time 21 Seconds
(without alignments)
622.574 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576
Sequence: 1 MVGFKATDVPPTATVTKFLGA.....TYEOLKRALMACTSRAPF 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA:*
2: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/BACKFILES1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1572	99.7	309	1	US-08-518-878B-51
2	1572	99.7	309	2	US-08-807-861A-51
3	1572	99.7	309	3	US-08-470-868A-51
4	1572	99.7	309	3	US-09-210-681-51
5	1572	99.7	309	3	US-08-946-719A-51
6	1572	99.7	309	4	US-09-547-983-51
7	1520	96.4	299	1	US-08-518-878B-56
8	1520	96.4	299	2	US-08-470-868A-56
9	1282	81.3	303	1	US-08-294-522B-36
10	1279	81.2	303	1	US-08-518-878B-37
11	1279	81.2	303	1	US-08-807-861A-37
12	1279	81.2	303	2	US-08-470-868A-37
13	1279	81.2	303	3	US-09-210-681-37
14	1279	81.2	303	3	US-08-946-719A-37
15	1279	81.2	303	4	US-09-547-983-37
16	1178.5	74.8	308	2	US-08-937-466-2
17	1178.5	74.8	308	2	US-09-172-528-2
18	1178.5	74.8	308	3	US-09-318-199-2
19	1178.5	74.8	308	3	US-09-503-579-2
20	1162.5	73.8	432	2	US-08-937-466-4
21	1162.5	73.8	432	2	US-09-172-528-4
22	1162.5	73.8	432	3	US-09-318-199-4
23	1162.5	73.8	432	3	US-09-503-579-4
24	1149.5	72.9	312	3	US-09-142-565-2
25	967.5	61.4	256	2	US-08-937-466-6
26	967.5	61.4	256	2	US-09-172-528-6
27	967.5	61.4	256	3	US-09-318-199-6

28	967.5	61.4	256	3	US-09-503-579-6	Sequence 6, Appl
29	915.5	58.1	307	2	US-08-807-861A-56	Sequence 56, Appl
30	915.5	58.1	307	3	US-09-210-681-56	Sequence 56, Appl
31	915.5	58.1	307	3	US-08-946-719A-56	Sequence 56, Appl
32	915.5	58.1	307	4	US-09-547-983-56	Sequence 56, Appl
33	894.5	56.8	306	5	PCT-US94-09799-1	Sequence 1, Appl
34	521.5	33.1	335	4	US-09-482-273-118	Sequence 118, App
35	519	32.9	291	4	US-09-501-558-2	Sequence 2, Appl
36	401	25.4	293	4	US-09-501-558-4	Sequence 4, Appl
37	337	21.4	95	3	US-09-142-565-6	Sequence 6, Appl
38	288	18.3	308	4	US-09-599-360B-91	Sequence 91, Appl
39	273	17.3	311	2	US-08-775-009-32	Sequence 32, Appl
40	273	17.3	311	2	US-08-775-009-32	Sequence 32, Appl
41	271	17.2	325	4	US-09-489-847-155	Sequence 155, App
42	256	16.2	320	2	US-08-933-750C-12	Sequence 12, Appl
43	256	16.2	320	3	US-09-234-613-12	Sequence 12, Appl
44	254.5	16.1	298	4	US-09-434-354-49	Sequence 49, Appl
45	252	16.0	74	3	US-09-142-565-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Targila, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518, 878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66145 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-51
Query Match 99.7%; Score 1572; DB 1; Length 309;
Best Local Similarity 99.7%; Pred. No. 4.9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVGFKATDVPPTATVTKFLGAGTACIADLLIFPLDTAKVRILQIGESGSPVRAASQYR 60
DB 1 MVGFKATDVPPTATVTKFLGAGTACIADLLIFPLDTAKVRILQIGESGSPVRAASQYR 60
QY 61 GVGKTLTVWRTEGPRSLVNGLVAGLQROMSPASVRIQLYDSVXQFYTKSEHSASISRL 120

DB 61 GWMGILTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTKSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAPPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
QY 181 PNVAARNALVNCALVTVYDLIKDALLKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
DB 181 PNVAARNALVNCALVTVYDLIKDALLKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
QY 241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVYTHQKRALMA 300
DB 241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVYTHQKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 2

US-08-807-861A-51
Sequence 51, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-51

Query Match 99.7%; Score 1572; DB 2; Length 309;
Best Local Similarity 99.7%; Pred. No. 4.9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFKATDVPTATVVKELGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60

DB 1 GWMGILTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTKSEHASIGSRL 120
QY 61 GWMGILTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTKSEHASIGSRL 120
DB 61 GWMGILTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTKSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAPPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
QY 181 PNVAARNALVNCALVTVYDLIKDALLKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
DB 181 PNVAARNALVNCALVTVYDLIKDALLKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
QY 241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVYTHQKRALMA 300
DB 241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRLGSMNVVMFVYTHQKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 3

US-08-470-868A-51
Sequence 51, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-51

Query Match 99.7%; Score 1572; DB 2; Length 309;
Best Local Similarity 99.7%; Pred. No. 4.9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFKATDVPTATVVKELGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
DB 1 MVGFKATDVPTATVVKELGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60

QY 61 GWMGTTLMVTEGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSESHASISRL 120
DB 61 GWMGTTLMVTEGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSESHASISRL 120
QY 121 LAGSTTGALAAVAAQPTDVVKRFOQAQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAQPTDVVKRFOQAQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNALVNCALVLYDILKDALIKANLMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
DB 181 PNVARNALVNCALVLYDILKDALIKANLMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
QY 241 RYMNSALQYSSAGHCALMTLQKGPRAFYKGFMPSPFLRGSNNVWFVYEQKRALMA 300
DB 241 RYMNSALQYSSAGHCALMTLQKGPRAFYKGFMPSPFLRGSNNVWFVYEQKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 4

US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-210-681-51

Query Match 99.7%; Score 1572; DB 3; Length 309;
Best Local Similarity 99.7%; Pred. No. 4,9e-168;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MUGFRATVPPLATATKFLGAGTACIADLTFFPDLTAKVRLQIGESQGPVATASQYR 60
DB 1 MUGFRATVPPLATATKFLGAGTACIADLTFFPDLTAKVRLQIGESQGPVATASQYR 60
QY 61 GWMGTTLMVTEGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSESHASISRL 120
DB 61 GWMGTTLMVTEGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSESHASISRL 120
QY 121 LAGSTTGALAAVAAQPTDVVKRFOQAQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAQPTDVVKRFOQAQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNALVNCALVLYDILKDALIKANLMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
DB 181 PNVARNALVNCALVLYDILKDALIKANLMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
QY 241 RYMNSALQYSSAGHCALMTLQKGPRAFYKGFMPSPFLRGSNNVWFVYEQKRALMA 300
DB 241 RYMNSALQYSSAGHCALMTLQKGPRAFYKGFMPSPFLRGSNNVWFVYEQKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 5

US-08-946-719A-51
Sequence 51, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid

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Page 4

STRANDEDNESS: single
TOPOLOGY: unknown
US-08-946-719A-51

Query Match 99.7%; Score 1572; DB 3; Length 309;
Best Local Similarity 99.7%; Pred. No. 4,9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWGFKATVPPTATKFLGAGTACIADLITFPDIAKVRLOIQESOGPVATASQYR 60
DB 1 MWGFKATVPPTATKFLGAGTACIADLITFPDIAKVRLOIQESOGPVATASQYR 60
QY 61 GWMGTLTMTREGRSLNGLVAGLQOMSFASVRIGLYDSVKQPTKSEHASIGSL 120
DB 61 GWMGTLTMTREGRSLNGLVAGLQOMSFASVRIGLYDSVKQPTKSEHASIGSL 120
QY 121 LAGSTTGALAVAAOPTDVYKVRFOQABAGGRRYQSTVNAKTIABEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAOPTDVYKVRFOQABAGGRRYQSTVNAKTIABEGFRGLMKGTS 180
QY 181 PNVAARNAIVNCAELVYDILKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
DB 181 PNVAARNAIVNCAELVYDILKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
QY 241 RYMNSALGOYSAGHCHLTMLOKESPRAFYKGFMSFLRGSNNVVMFTYEQLRALMA 300
DB 241 RYMNSALGOYSAGHCHLTMLOKESPRAFYKGFMSFLRGSNNVVMFTYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 6
US-09-547-983-51

Sequence 51, Application US/09547983
Patent No. 65,8402

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/547,983

FILING DATE: 12-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/807,861

FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

US-09-547-983-51
SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Query Match 99.7%; Score 1572; DB 4; Length 309;
Best Local Similarity 99.7%; Pred. No. 4,9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWGFKATVPPTATKFLGAGTACIADLITFPDIAKVRLOIQESOGPVATASQYR 60
DB 1 MWGFKATVPPTATKFLGAGTACIADLITFPDIAKVRLOIQESOGPVATASQYR 60
QY 61 GWMGTLTMTREGRSLNGLVAGLQOMSFASVRIGLYDSVKQPTKSEHASIGSL 120
DB 61 GWMGTLTMTREGRSLNGLVAGLQOMSFASVRIGLYDSVKQPTKSEHASIGSL 120
QY 121 LAGSTTGALAVAAOPTDVYKVRFOQABAGGRRYQSTVNAKTIABEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAOPTDVYKVRFOQABAGGRRYQSTVNAKTIABEGFRGLMKGTS 180
QY 181 PNVAARNAIVNCAELVYDILKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
DB 181 PNVAARNAIVNCAELVYDILKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
QY 241 RYMNSALGOYSAGHCHLTMLOKESPRAFYKGFMSFLRGSNNVVMFTYEQLRALMA 300
DB 241 RYMNSALGOYSAGHCHLTMLOKESPRAFYKGFMSFLRGSNNVVMFTYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 7

US-08-518-878B-56

Sequence 56, Application US/08518878B

Patent No. 5,702,902

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/518,878B

FILING DATE: 23-AUG-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-036

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-8788-56

Query Match 96.4%; Score 1520; DB 1; Length 299;
Best Local Similarity 99.7%; Pred. No. 3.2e-162;
Matches 298; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTAIVKFLAGTACIADLITFPDITAKVRLQIOGSGQPVRAATASQYRGVMTILTMV 70
DB 1 PTAIVKFLAGTACIADLITFPDITAKVRLQIOGSGQPVRAATASQYRGVMTILTMV 60
QY 71 RTEGPRSLYNGVLAQLOQMSFASVRIQLYDSVKQPTKGSSEHISRLLAGSTTGALA 130
DB 61 RTEGPRSLYNGVLAQLOQMSFASVRIQLYDSVKQPTKGSSEHISRLLAGSTTGALA 120
QY 131 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPVARNALVN 190
DB 121 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPVARNALVN 180
QY 191 CAELVTVYDLIKDALLKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYNSALGQY 250
DB 181 CAELVTVYDLIKDALLKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYNSALGQY 240
QY 251 SSAGHCALTMLQKEGPRAFYKGFMPFRLGSMNVVMFVTVYEQLRALMAACTSREAPF 309
DB 241 SSAGHCALTMLQKEGPRAFYKGFMPFRLGSMNVVMFVTVYEQLRALMAACTSREAPF 299

RESULT 8
US-08-470-868A-56
Sequence 56, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF OBESITY: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

Query Match 96.4%; Score 1520; DB 2; Length 299;
Best Local Similarity 99.7%; Pred. No. 3.2e-162;
Matches 298; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTAIVKFLAGTACIADLITFPDITAKVRLQIOGSGQPVRAATASQYRGVMTILTMV 70
DB 1 PTAIVKFLAGTACIADLITFPDITAKVRLQIOGSGQPVRAATASQYRGVMTILTMV 60
QY 71 RTEGPRSLYNGVLAQLOQMSFASVRIQLYDSVKQPTKGSSEHISRLLAGSTTGALA 130
DB 61 RTEGPRSLYNGVLAQLOQMSFASVRIQLYDSVKQPTKGSSEHISRLLAGSTTGALA 120
QY 131 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPVARNALVN 190
DB 121 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPVARNALVN 180
QY 191 CAELVTVYDLIKDALLKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYNSALGQY 250
DB 181 CAELVTVYDLIKDALLKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYNSALGQY 240
QY 251 SSAGHCALTMLQKEGPRAFYKGFMPFRLGSMNVVMFVTVYEQLRALMAACTSREAPF 309
DB 241 SSAGHCALTMLQKEGPRAFYKGFMPFRLGSMNVVMFVTVYEQLRALMAACTSREAPF 299

RESULT 9
US-08-294-522B-36
Sequence 36, Application US/08294522B
Patent No. 5741666
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF OBESITY: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-8711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-294-522B-36

Query Match 81.3%; Score 1282; DB 1; Length 303;
Best Local Similarity 85.4%; Pred. No. 1.7e-115;
Matches 264; Conservative 12; Mismatches 27; Indels 6; Gaps 6;

QY 1 MVGFKATDVPTATVYKFLAGTACIADLITFPDITAKVRLQIOGSGQPVRAATASQYR 60
DB 1 MVGFKATDVPTATVYKFLAGTACIADLITFPDITAKVRLQIOGSGQPVRAATASQYR 60

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QY 61 GVMGTLTMTWTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVQKPYTKSEHAGISRL 120
DB 61 GVLGTLTMTWTEGPRSLYNGLVAGLQROMSLASVRIGLYDSVQKPYTKSEHAGISRL 120
QY 121 LAGSTGALAAVVAQPTDVVKVFPQAAGGRRYOSTVNAKYTIAREEGFRLMKGTS 180
DB 121 LAGSTGALAAVVAQPTDVVKVFPQAAGGRRYOSTVNAKYTIAREEGFRLMKGTS 178
QY 181 PNVARNAIVCAELVYDILKDALIKANLMTDLPCHFTSAFGAGFCTTVIASPVDVYKT 240
DB 179 -QCARNAIIVCAELVYDILKDTLL-SHMTDLPCHFTSAFGAGFCTTVIASPVDVYKT 236
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLGSMNVVMFVYEQLRALMA 300
DB 237 RYM-TLLGQYHSGHCALT-CSEEGPALFNQGVMPSPFLGSMNVVMFVYEQLRALMA 294
QY 301 ACTSREAPF 309
DB 295 AYGSRAPF 303

RESULT 10
US-08-518-878B-37
Sequence 37, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518-878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-37

Query Match 81.2%; Score 1279; DB 1; Length 303;
Best Local Similarity 85.1%; Pred. No. 3.7e-135;
Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

QY 121 LAGSTGALAAVVAQPTDVVKVFPQAAGGRRYOSTVNAKYTIAREEGFRLMKGTS 180
DB 121 LAGSTGALAAVVAQPTDVVKVFPQAAGGRRYOSTVNAKYTIAREEGFRLMKGTS 178
QY 181 PNVARNAIVCAELVYDILKDALIKANLMTDLPCHFTSAFGAGFCTTVIASPVDVYKT 240
DB 179 -QCARNAIIVCAELVYDILKDTLL-SHMTDLPCHFTSAFGAGFCTTVIASPVDVYKT 236
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLGSMNVVMFVYEQLRALMA 300
DB 237 RYM-TLLGQYHSGHCALT-CSEEGPALFNQGVMPSPFLGSMNVVMFVYEQLRALMA 294
QY 301 ACTSREAPF 309
DB 295 AYGSRAPF 303

RESULT 11
US-08-807-861A-37
Sequence 37, Application US/08807861A
Patent No. 3853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-37

Query Match 81.2%; Score 1279; DB 2; Length 303;
Best Local Similarity 85.1%; Pred. No. 3.7e-135;
Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

QY 1 MVGFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGSOGPYRTASAGYR 60
DB 1 MVGFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGSOGPYRTASAGYR 60

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QY 6 GWNGLTLTWRRREGPSL:YNGLVAG:JORMSASVARI:LYDSVKQFTYKXSEHASIGSRL 120
 Db 61 GUGGTLTWRRREGPSL:YNGLVAG:JORMSLASVARI:LYDSVKQFTYKXSEHGIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVYKVR:FQAQAPAGGGRPYRQSTVNAVYKTAREEGFRGLMKGTS 180
 Db 121 LAGSTTGALAVAAQPTDVYKVR:FQAQAGGGRPYRA-LSSYNKTR-GGIRGLMKGLS 178
 QY 181 PNVAARNAIVNCAELVYDILIKDALLKANIMTDULCHEFTSAFGAGFCCTVYASVDVYKT 240
 Db 179 -QCARNAIVNCAELVYDILIKDTLL-SHMTDDULCHEFTSAFGAGFCCTVYASVDVYKT 236
 QY 241 RYNSASLGGYSAGHCALTMLOKEGPRAFYKGFMEFLUGSMNVMEFVYEQLRALMA 300
 Db 237 RYM-TLLGGYSAGHCALT-CSEEGPALFNQGVMPSEFLRLSNMVMVFVYEQLRALMA 294
 QY 301 ACTSREAPF 309
 Db 295 AYQSRAPF 303

RESULT 12
 US-08-470-868A-37
 Sequence 37, Application US/08470868A
 Patent No. 5861495
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis C.
 TITLE OF INVENTION: Compositions and Methods for the
 TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie and Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,868A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-0031-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66441 PENNIE
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 303 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-08-470-868A-37

Query Match	81.2%;	Score 1279;	DB 2;	Length 303;
Best Local Similarity	85.1%;	Pred. No. 3.7e-135;		
Matches 263;	Conservative 13;	Mismatches 27;	Indels 6;	Gaps 6;

QY MGEFKATDVEPNTATVYFGLAGTACTATLTFEPDITAKVRLQIGSSQGVATASACQR 60

Db 1 MGEFKATDVEPNTATVYFGLAGTACTATLTFEPDITAKVRLQIGSSQGVATASACQR 60

QY 61 GYMGITLIMVRLEGPSLYNLVAGLQDQMSFASVRLGLDYSVKQPTKQSEHASTGSL 120

D6 6. GVLGTLITWVRREGPRSLNYNGLVAGLQJEMSLASVRLIGLDVDSVQFPTKSGEHGIGSRL 120

QY 121 LAGSTTGALAAVAQPTDVVKYRFPQAQARACGGRRYOSTYNAKYTTIRAREGFGFLMKGTS 180

D6 121 LAGSTTGALAAVAQPTDVVKYRFPQAPRAGGGRYRA-LSSYKNITR-GGIGLWKGJS 178

QY 181 PNVARNAIYNCAELVTYDLIKDALIKANIMTDDLPCHFTSAFGAGFCTTVIASPVDVVKI 240

D6 179 -QCARNAIYNCAELVTYDLIKDTLL-SHLMDDLPCHFTSAFGAGFCTTVIASPVDVVKI 236

QY 241 RYNSALSGYSSAGHCALMTQKGGRAFYFGMPSPFLGASNNVVFVTEYLKRALMA 300

D6 237 RYV-TLLGGYHSHAGHCALT-CSEEGPALFNQGVMPSPFLGASNNVVFVTEYLORALMA 294

QY 301 ACTSREAPF 309

D6 295 AYQSRAPF 303

ESULT 13
S-09-210-681-37
Sequence 37, Application US/09210681

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITILE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210.681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

LEENA: 00141 FENNIE
INFORMATION FOR SEQ ID NO: 37:

LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single

Query Match	81.2%;	Score 1279;	DB 3;	Length 303;
Best Local Similarity	85.1%;	Pred. No. 3.7e-135;		
Matches 263;	Conservative 13;	Mismatches 27;	Indels 6;	Gaps 6;

Fri Feb 6 16:59:26 2004

us-09-884-814-1.rai

Page 8

QY 1 MWGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
Db 1 MWGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
QY 61 GWMGTILTMVTEGPRSLVNGLVAGLQRFQSPASVIRGLYDSVKQFYTKGSEHAGISRL 120
Db 61 GVLGTILTMVTEGPRSLVNGLVAGLQRFQSPASVIRGLYDSVKQFYTKGSEHAGISRL 120
QY 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
Db 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
QY 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
Db 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
QY 181 PNVARNATVNCALVTVYDLIKDALIKANLMTDDLPCHFPSAFGAGFCTTVIASPVDVYKT 240
Db 179 -OCARNAIVNCALVTVYDLIKDALIKANLMTDDLPCHFPSAFGAGFCTTVIASPVDVYKT 236
QY 241 RYNNALGOYSAGHCALTMLOKSGPRAFYKGFMPSEFLRGSNNVVMFVYEQLOKALMA 300
Db 237 RYM-TLIGQYHSAGHCALT-CSBEGPALFNQGVMPSEFLRGSNNVVMFVYEQLOKALMA 294
QY 301 ACTSREAPF 309
Db 295 AYGSRREAPF 303

RESULT 14

US-08-946-719A-37
Sequence 37, Application US/08946719A
Patent No. 6121017

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,719A

FILING DATE: 8-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/807,861

FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 869-9741/8864

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 303 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

US-08-946-719A-37

Query Match 81.2%; Score 1279; DB 3; Length 303;
Best Local Similarity 85.1%; Pred. No. 3,7e-135;

Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

QY 1 MWGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
Db 1 MWGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
QY 61 GWMGTILTMVTEGPRSLVNGLVAGLQRFQSPASVIRGLYDSVKQFYTKGSEHAGISRL 120
Db 61 GVLGTILTMVTEGPRSLVNGLVAGLQRFQSPASVIRGLYDSVKQFYTKGSEHAGISRL 120
QY 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
Db 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
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Db 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQSTVNAKYTIAREGFRGLMKGTS 180
QY 181 PNVARNATVNCALVTVYDLIKDALIKANLMTDDLPCHFPSAFGAGFCTTVIASPVDVYKT 240
Db 179 -OCARNAIVNCALVTVYDLIKDALIKANLMTDDLPCHFPSAFGAGFCTTVIASPVDVYKT 236
QY 241 RYNNALGOYSAGHCALTMLOKSGPRAFYKGFMPSEFLRGSNNVVMFVYEQLOKALMA 300
Db 237 RYM-TLIGQYHSAGHCALT-CSBEGPALFNQGVMPSEFLRGSNNVVMFVYEQLOKALMA 294
QY 301 ACTSREAPF 309
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RESULT 15

US-09-547-983-37
Sequence 37, Application US/09547983
Patent No. 6518402

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/547,983

FILING DATE: 12-APR-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/807,861

FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 869-9741/8864

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

Fri Feb 6 16:59:26 2004

us-09-884-814-1.ral

/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-547-983-37

Query Match 81.2%; Score 1279; DB 4; Length 303;
Best Local Similarity 85.1%; Pred. No. 3.7e-135;
Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

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DB 1 MVEFKATDVPEPTATVVKFLGAGTACIADLITFPLDTAKVRLQIQESQGLVRTASAAQYR 60
QY 61 GVMGTITLMTRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFTYKGSRHASIGSRL 120
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DB 121 IAGSTGALAVVAAOPTDVYKVFQAPGAGGGRYRA-LSSYKNITR-GGIRGLMKGLS 178
QY 181 PNVARNAIVNCAELVYDILKDALLKANIMTDDLPGHFTSAFGAGCTTVIASPVVYKT 240
DB 179 -QCARNAIVNCAELVYDILKDTLL-SHIMTDDLPGHFTSAFGAGCTTVIASPVVYKT 236
QY 241 RYNNASALGOYSSAGHCALFTWLQKEGPRAFYKGFMPSEFLIGSMNVVMFTYEQLKRALMA 300
DB 237 RYM-TLIGQTHSAGHCALT-CSDEGPALFNQGVMPSEFLIGSMNVVMFTYEQLQORALMA 294
QY 301 ACTSREAPF 309
DB 295 AYOQREAPF 303

Search completed: February 4, 2004, 09:20:29
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 09:19:29 ; Search time 34 Seconds

(without alignments)
1902.915 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576

Sequence: 1 MVEFKATDVPPRTATVFLGA.....TYEQKRALMACTSRAPF 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1576	100.0	309	US-10-270-861-34	Sequence 34, Appli
3	1576	100.0	314	US-10-265-689-1	Sequence 1, Appli
4	1576	100.0	314	US-09-823-886A-4	Sequence 4, Appli
5	1572	99.7	309	US-09-884-814-6	Sequence 6, Appli
6	1570	99.6	309	US-09-884-814-8	Sequence 8, Appli
7	1570	99.6	309	US-10-197-019-3	Sequence 3, Appli
8	1570	99.6	309	US-10-001-051B-2	Sequence 2, Appli
9	1145.5	72.9	312	US-09-734-134-2	Sequence 2, Appli
10	1145.5	72.9	312	US-09-826-507-2	Sequence 2, Appli
11	1145.5	72.9	312	US-09-808-457-2	Sequence 2, Appli
12	1101.5	69.9	300	US-10-270-861-35	Sequence 35, Appli
13	998.5	63.4	275	US-09-808-457-4	Sequence 4, Appli
14	998.5	63.4	284	US-09-823-886A-6	Sequence 6, Appli
15	915	58.1	307	US-09-823-886A-2	Sequence 2, Appli

16	907	57.6	307	US-10-270-861-33	Sequence 33, Appli
17	521.5	33.1	322	US-10-270-861-7	Sequence 7, Appli
18	521.5	33.1	325	US-10-270-861-1	Sequence 1, Appli
19	521.5	33.1	335	US-09-984-271-118	Sequence 118, App
20	517.5	32.8	322	US-10-270-861-11	Sequence 11, Appli
21	517.5	32.8	325	US-10-270-861-13	Sequence 13, Appli
22	510	32.4	291	US-10-108-260A-2476	Sequence 2476, App
23	496	31.5	353	US-10-270-861-9	Sequence 9, Appli
24	473.5	30.0	323	US-09-946-374-406	Sequence 406, App
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27	473.5	30.0	323	US-10-006-130A-406	Sequence 406, App
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29	473.5	30.0	323	US-10-015-392A-406	Sequence 406, App
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33	473.5	30.0	323	US-10-063-586-126	Sequence 126, App
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35	473.5	30.0	323	US-10-017-867A-406	Sequence 406, App
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37	473.5	30.0	323	US-10-063-514-126	Sequence 126, App
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40	473.5	30.0	323	US-10-063-527-126	Sequence 126, App
41	473.5	30.0	323	US-10-063-528-126	Sequence 126, App
42	473.5	30.0	323	US-10-063-529-126	Sequence 126, App
43	473.5	30.0	323	US-10-063-536-126	Sequence 126, App
44	473.5	30.0	323	US-10-063-540-126	Sequence 126, App
45	473.5	30.0	323	US-10-063-546-126	Sequence 126, App

ALIGNMENTS

RESULT 1

US-09-884-814-1

Sequence 1, Application US/09884814

Patent No. US20020127600A1

GENERAL INFORMATION:

APPLICANT: Chen, Jin-Long

APPLICANT: Amarel, M. Catherine

APPLICANT: Tularik Inc.

TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and Methods of Use

FILE REFERENCE: 018781-00110US

CURRENT APPLICATION NUMBER: US/09/884,814

CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: US 09/124,293

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 309

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)

US-09-884-814-1

Query Match 100.0%; Score 1576; DB 10; Length 309;

Best Local Similarity 100.0%; Pred. No. 3.3e-157;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MVEFKATDVPPRTATVFLGAGTAACIADITPPLDTAKVRLIQESOGPYRATSAQYR 60

Cy 61 GVGKTLITWRTGPRSLYNGLVAGLQROMSTASVRIGLYDSVKQFYTKGSEHHSIGRL 120

Db 61 GVGKTLITWRTGPRSLYNGLVAGLQROMSTASVRIGLYDSVKQFYTKGSEHHSIGRL 120

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Db      121 LAGSTTGALAAVAAPPTDVVKRFQARAGGRKYOSTVNAKYTIAREEGFGLMKGS 180
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Db      181 PNVARNALVNCALVETVYDLIKDALIKANLMTDDLPCHTSAFGAGCTTVIASPVDVVK 240
Qy      241 RYMSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVNVVFVTEYEQKRALMA 300
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Qy      301 ACTSREAPF 309
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RESULT 2

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US-10-270-861-34
; Sequence 34, Application US/10270861
; Publication No. US20030077749A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Pan, James
; TITLE OF INVENTION: UCPS
; FILE REFERENCE: P1663R2
; CURRENT APPLICATION NUMBER: US/10/270,861
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/433,622
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/110,286
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/129,583
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: US 60/143,886
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 34
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-270-861-34

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Query Match      100.0%; Score 1576; DB 15; Length 309;
Best Local Similarity 100.0%; Pred. No. 3,3e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 GWMGTILTMVTEGPRSLVNGLVAGIQROMSFASVRIGLYDSVKQFTYKSGSEHASISRL 120
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Qy      181 PNVARNALVNCALVETVYDLIKDALIKANLMTDDLPCHTSAFGAGCTTVIASPVDVVK 240
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RESULT 3
US-10-265-689-1

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; Sequence 1, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SUMMIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICOUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-265-689-1

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Query Match      100.0%; Score 1576; DB 15; Length 309;
Best Local Similarity 100.0%; Pred. No. 3,3e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MWGFKATDVPTATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESQGPVATASAOYR 60
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Qy      61 GWMGTILTMVTEGPRSLVNGLVAGIQROMSFASVRIGLYDSVKQFTYKSGSEHASISRL 120
Db      61 GWMGTILTMVTEGPRSLVNGLVAGIQROMSFASVRIGLYDSVKQFTYKSGSEHASISRL 120
Qy      121 LAGSTTGALAAVAAPPTDVVKRFQARAGGRKYOSTVNAKYTIAREEGFGLMKGS 180
Db      121 LAGSTTGALAAVAAPPTDVVKRFQARAGGRKYOSTVNAKYTIAREEGFGLMKGS 180
Qy      181 PNVARNALVNCALVETVYDLIKDALIKANLMTDDLPCHTSAFGAGCTTVIASPVDVVK 240
Db      181 PNVARNALVNCALVETVYDLIKDALIKANLMTDDLPCHTSAFGAGCTTVIASPVDVVK 240
Qy      241 RYMSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVNVVFVTEYEQKRALMA 300
Db      241 RYMSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRIGSNVNVVFVTEYEQKRALMA 300
Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

```

RESULT 4

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US-09-823-886A-4
; Sequence 4, Application US/09823886A
; Publication No. US20030150022A1
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha
; APPLICANT: Berry-Lowe, Sandra
; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
; FILE REFERENCE: C1102/7002
; CURRENT APPLICATION NUMBER: US/09/823,886A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,553
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 314

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-886A-4

Query Match          100.0%; Score 1576; DB 12; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.4e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKVRLIQESOGPYRATASQYR 60
DB 6 MGGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKVRLIQESOGPYRATASQYR 65
QY 61 GVGGTILLWRTGSPSLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 66 GVGGTILLWRTGSPSLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 125
QY 121 LAGSTTGALAAVAAPPTDVYKVFQQAAPAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
DB 126 LAGSTTGALAAVAAPPTDVYKVFQQAAPAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 185
QY 181 PNVARNAIVNCAELVTVYDLIKALLKANIMTDDLPCHTSAFGAGFCTTVIASPVYVKT 240
DB 186 PNVARNAIVNCAELVTVYDLIKALLKANIMTDDLPCHTSAFGAGFCTTVIASPVYVKT 245
QY 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVMEVTEYEQLRALMA 300
DB 246 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVMEVTEYEQLRALMA 305
QY 301 ACTSREAPF 309
DB 306 ACTSREAPF 314

RESULT 5
US-09-884-814-6
; Sequence 6, Application US/09884814
; Patent No. US20020127600A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-00110US
; CURRENT APPLICATION NUMBER: US/09/884,814
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tartaglia et al.
US-09-884-814-6

Query Match          99.7%; Score 1572; DB 10; Length 309;
Best Local Similarity 99.7%; Pred. No. 8.7e-157;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKVRLIQESOGPYRATASQYR 60
DB 1 MGGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKVRLIQESOGPYRATASQYR 60
QY 61 GVGGTILLWRTGSPSLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVGGTILLWRTGSPSLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVYKVFQQAAPAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAPPTDVYKVFQQAAPAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
```

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QY 181 PNVARNAIVNCAELVTVYDLIKALLKANIMTDDLPCHTSAFGAGFCTTVIASPVYVKT 240
DB 181 PNVARNAIVNCAELVTVYDLIKALLKANIMTDDLPCHTSAFGAGFCTTVIASPVYVKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVMEVTEYEQLRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVMEVTEYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 6
US-09-884-814-8
; Sequence 8, Application US/09884814
; Patent No. US20020127600A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-00110US
; CURRENT APPLICATION NUMBER: US/09/884,814
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.
US-09-884-814-8

Query Match          99.6%; Score 1570; DB 10; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.4e-156;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKVRLIQESOGPYRATASQYR 60
DB 1 MGGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKVRLIQESOGPYRATASQYR 60
QY 61 GVGGTILLWRTGSPSLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVGGTILLWRTGSPSLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVYKVFQQAAPAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAPPTDVYKVFQQAAPAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
QY 181 PNVARNAIVNCAELVTVYDLIKALLKANIMTDDLPCHTSAFGAGFCTTVIASPVYVKT 240
DB 181 PNVARNAIVNCAELVTVYDLIKALLKANIMTDDLPCHTSAFGAGFCTTVIASPVYVKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVMEVTEYEQLRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVMEVTEYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 7
US-10-197-019-3
; Sequence 3, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-019-3

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Query Match          99.6%; Score 1570; DB 12; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.4e-156;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 1 MGGKATDVPPATATKFLGAGTACIADLITPDLTAKRLOIQESQGPVATASAOYR 60
DB 1 MGGKATDVPPATATKFLGAGTACIADLITPDLTAKRLOIQESQGPVATASAOYR 60
QY 61 GWMGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRGLWKGTG 180
DB 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRGLWKGTG 180
QY 181 PNVARNAIVNCAELVYDILKDALLKANLMTDDLPCHEFSAFGAGCTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCAELVYDILKDALLKANLMTDDLPCHEFSAFGAGCTTVIASPVDVYKT 240
QY 241 RYNSALGQYSSAGHCALITMLQKEGPRAFYKGFMPSPFLRGSWNVVMTVYEQLRALMA 300
DB 241 RYNSALGQYSSAGHCALITMLQKEGPRAFYKGFMPSPFLRGSWNVVMTVYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

```

RESULT 8

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US-10-001-051B-2
; Sequence 2, Application US/10001051B
; Publication No. US20020172588A1
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Mirella
; APPLICANT: Shamloo, Mehdiad
; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Wielech, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: AGY Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
; TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
; FILE REFERENCE: 019488-003010US
; CURRENT APPLICATION NUMBER: US/10/001,051B
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Unknown Organism

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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
US-10-001-051B-2

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```

Query Match          99.6%; Score 1570; DB 14; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.4e-156;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MGGKATDVPPATATKFLGAGTACIADLITPDLTAKRLOIQESQGPVATASAOYR 60
DB 1 MGGKATDVPPATATKFLGAGTACIADLITPDLTAKRLOIQESQGPVATASAOYR 60
QY 61 GWMGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRGLWKGTG 180
DB 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRGLWKGTG 180
QY 181 PNVARNAIVNCAELVYDILKDALLKANLMTDDLPCHEFSAFGAGCTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCAELVYDILKDALLKANLMTDDLPCHEFSAFGAGCTTVIASPVDVYKT 240
QY 241 RYNSALGQYSSAGHCALITMLQKEGPRAFYKGFMPSPFLRGSWNVVMTVYEQLRALMA 300
DB 241 RYNSALGQYSSAGHCALITMLQKEGPRAFYKGFMPSPFLRGSWNVVMTVYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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RESULT 9

```

US-09-734-134-2
; Sequence 2, Application US/09734134
; Patent No. US20010010929A1
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James Godden
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002-D1
; CURRENT APPLICATION NUMBER: US/09/734,134
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: GB 9704551.2
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: GB 9705614.7
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: EP 97305305.1
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: GB 9800633
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 09/142,565
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-734-134-2

```

```

Query Match          72.2%; Score 1149.5; DB 9; Length 312;
Best Local Similarity 72.2%; Pred. No. 2.5e-112;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

```

```

QY 1 MGGKATDVPPATATKFLGAGTACIADLITPDLTAKRLOIQESQGPVATASAOYR 60
DB 1 MGGKATDVPPATATKFLGAGTACIADLITPDLTAKRLOIQESQGPVATASAOYR 60
QY 61 GWMGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120

```

```
Db 60 GVLGTLTMTVRTEGCPSPYNGLVAGLQROMSPASIRILGYDSVQVYTPKCADNSLTLTR 119
QY 120 LLAGSTTGALAAVAVOPTDVVVRFOQAARAG---GGRYQSTYVNAVYTTAREGPGGLM 176
Db 120 LLAGCTTGAMAVTCQAPTDVAVVRFOASIHGSPSRDKYSGTMDAKRTIAREGAVGLM 179
QY 177 KGTSPNVAANAIVNCAELVYTDILDKALLKANLMTDLPCHFTSAFGAGCTTVIASPVD 236
Db 180 KGTLPNIMRNAIVNCAEVYTDILKEKLLDYLTDNFPCHFVSAFGAGCATVVASPVD 239
QY 237 VKTRYNMSALGOYSAGHCALTMQXGPRAPFYKGMPSFLRLGSMNVVVFVTEQLR 236
Db 240 VKTRYNMSPPGQYFSPDLCMKIMVAQSGPFAFYKGFPSFLRLGSMNVVVFVTEQLR 239
QY 297 ALMAACTSREAPF 309
Db 300 ALMKVQMLRESPE 312
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RESULT 10

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US-09-826-507-2
; Sequence 2, Application US/09826507
; Patent No. US20020004492A1
; GENERAL INFORMATION:
; APPLICANT: Lee James Bealey
; APPLICANT: John Christopher Clapham
; APPLICANT: Robert James Godden
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: GH-9009-C1
; CURRENT APPLICATION NUMBER: US/09/826,507
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/312,620
; PRIOR FILING DATE: 1998-05-17
; PRIOR APPLICATION NUMBER: 9814926.3
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 312
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-507-2
```

```
Query Match 72.9%; Score 1149.5; DB 9; Length 312;
Best Local Similarity 72.2%; Pred. No. 2.5e-112;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;
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```
QY 1 MNGFATDVPPTATVKEFGAGTACIADLITPLDTAKVLOIQESGQPYRATASAOYR 60
Db 1 MNGLKPSDVPPTMAVKEFGAGTACIADLITPLDTAKVLOIQESGQPYRATASAOYR 59
QY 61 GVMGTLTMTVRTEGCPSPYNGLVAGLQROMSPASIRILGYDSVQVYTPKCADNSLTLTR 119
Db 60 GVLGTLTMTVRTEGCPSPYNGLVAGLQROMSPASIRILGYDSVQVYTPKCADNSLTLTR 119
QY 120 LLAGSTTGALAAVAVOPTDVVVRFOQAARAG---GGRYQSTYVNAVYTTAREGPGGLM 176
Db 120 LLAGCTTGAMAVTCQAPTDVAVVRFOASIHGSPSRDKYSGTMDAKRTIAREGAVGLM 179
QY 177 KGTSPNVAANAIVNCAELVYTDILDKALLKANLMTDLPCHFTSAFGAGCTTVIASPVD 236
Db 180 KGTLPNIMRNAIVNCAEVYTDILKEKLLDYLTDNFPCHFVSAFGAGCATVVASPVD 239
QY 237 VKTRYNMSALGOYSAGHCALTMQXGPRAPFYKGMPSFLRLGSMNVVVFVTEQLR 236
Db 240 VKTRYNMSPPGQYFSPDLCMKIMVAQSGPFAFYKGFPSFLRLGSMNVVVFVTEQLR 239
QY 297 ALMAACTSREAPF 309
Db 300 ALMKVQMLRESPE 312
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RESULT 11

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US-09-808-457-2
; Sequence 2, Application US/09808457
; Patent No. US20020065239A1
; GENERAL INFORMATION:
; APPLICANT: Boettcher, Brian
; APPLICANT: Caplan, Shari
; APPLICANT: Kaleko, Michael
; APPLICANT: Connolly, Sheila
; APPLICANT: Desai, Urvil
; APPLICANT: Slobergy, Eric
; TITLE OF INVENTION: Methods and Compositions for Treatment
; FILE REFERENCE: 4-3133A/USN
; CURRENT APPLICATION NUMBER: US/09/808,457
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/xxx,xxx
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Protein UCP3L
US-09-808-457-2
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```
Query Match 72.9%; Score 1149.5; DB 9; Length 312;
Best Local Similarity 72.2%; Pred. No. 2.5e-112;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;
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```
QY 1 MNGFATDVPPTATVKEFGAGTACIADLITPLDTAKVLOIQESGQPYRATASAOYR 60
Db 1 MNGLKPSDVPPTMAVKEFGAGTACIADLITPLDTAKVLOIQESGQPYRATASAOYR 59
QY 61 GVMGTLTMTVRTEGCPSPYNGLVAGLQROMSPASIRILGYDSVQVYTPKCADNSLTLTR 119
Db 60 GVLGTLTMTVRTEGCPSPYNGLVAGLQROMSPASIRILGYDSVQVYTPKCADNSLTLTR 119
QY 120 LLAGSTTGALAAVAVOPTDVVVRFOQAARAG---GGRYQSTYVNAVYTTAREGPGGLM 176
Db 120 LLAGCTTGAMAVTCQAPTDVAVVRFOASIHGSPSRDKYSGTMDAKRTIAREGAVGLM 179
QY 177 KGTSPNVAANAIVNCAELVYTDILDKALLKANLMTDLPCHFTSAFGAGCTTVIASPVD 236
Db 180 KGTLPNIMRNAIVNCAEVYTDILKEKLLDYLTDNFPCHFVSAFGAGCATVVASPVD 239
QY 237 VKTRYNMSALGOYSAGHCALTMQXGPRAPFYKGMPSFLRLGSMNVVVFVTEQLR 236
Db 240 VKTRYNMSPPGQYFSPDLCMKIMVAQSGPFAFYKGFPSFLRLGSMNVVVFVTEQLR 239
QY 297 ALMAACTSREAPF 309
Db 300 ALMKVQMLRESPE 312
RESULT 12
US-10-270-861-35
; Sequence 35, Application US/10270861
; Publication No. US2003007749A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Pan, James
; TITLE OF INVENTION: UCPS
; FILE REFERENCE: P166382
; CURRENT APPLICATION NUMBER: US/10/270,861
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/433,622
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/110,286
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/129,583
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? PRIOR FILING DATE: 1999-04-16
 ? PRIOR APPLICATION NUMBER: US 60/143,886
 ? PRIOR FILING DATE: 1999-07-15
 ? NUMBER OF SEQ ID NOS: 36
 ? SEQ ID NO: 35
 ? LENGTH: 300
 ? TYPE: SRT
 ? ORGANISM: Homo Sapien
 ? US-10-270-861-35

Query Match	69.98;	Score 1101.5;	DB 15;	Length 300;
Best Local Similarity	72.6%;	Pred. No. 2.7e-107;		
Matches 217; Conservative	30;	Mismatches 47;	Indels 5;	Gaps 3

QY 1 VKFVGATGATACIADILTFPLDPAKRYLQIQSGSQCPVATISAQVRGMGILLMWTG 74

Db 3 VKFVGATGATACFADILTFPLDPAKRYLQIQSGENQ-VQTAALVQVRGVLGITLMWTG 61

QY 75 PRSLYNGVLVAGLGRQMSFASVRIGLVDKCYEYT-KGSEHISIGRLIAGSTGALAAV 133

Db 62 PCSPYNGVLVAGLGRQMSFASIRIGLVDKCYQYTFPKGADNSLITRILAGCTGAMAVTC 121

QY 134 AQPDPVYKVFQQAQAAG--GGRRQOSVYVNAKYTLIAEEGSGILMGTSNNVNAIYV 190

Db 122 AQPDPVYKVFQMSIHGSPRSRDKRSGTMDIAKRIIAEBGVRGLMKGLPTNIRNAIYV 181

QY 191 CAELVYDILKDALKANLMTDLPCHFSASAQAQCTTVLASPRVDYKRRYNSALGOY 250

Db 182 CAELVYDILKELILYHILTDLPCHFSASAQAQCAITVASPVDYKIRYNSPBGQY 241

QY 251 SSAGCHALTMLOXEGPRLPYKGMPSFELGSSNNVMTVYVYQLKRALMAACISREAPF 309

Db 242 FSPDDCMIRKVAOEGPRLPYKGFTEFLGSSNNVMTVYVYQLKRALMKYMRBSFP 300

RESULT 13

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US-09-808-45/-4
/ Sequence 45, Application US/09808457
/ Patent No. US20020065239A1
/ GENERAL INFORMATION:
/ APPLICANT: Boettcher, Brian
/ APPLICANT: Caplan, Shari
/ APPLICANT: Kaleko, Michael
/ APPLICANT: Connelly, Sheila
/ APPLICANT: Desai, Urv
/ APPLICANT: Slosberg, Eric
/ TITLE OF INVENTION: Methods and Compositions For Treatment
/ TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy
/ FILE REFERENCE: 4-3153A/US
/ CURRENT APPLICATION NUMBER: US/09/808,457
/ CURRENT FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/XXX,XXX
/ PRIOR FILING DATE: 2000-03-15
/ NUMBER OF SEQ. ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 275
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Protein UCP3S
US-09-808-457-4

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[illegible]

D6 GVLGTLITMVRREGCSPYNGVLVAGLQGMSPASIRLGLDVSQVYVTPPGADNSSLTR 118

QY 120 LLAGSTTGALAVAVOPDPVVKFQQAQARG--GGRRYSTVNAKTLARBEGFGLM 176

D6 120 ILAGCTTGMAVTCQOPDPDVVKVRQASIHGSPSRDKYSGTMDAARTLARBEGVNGLM 179

QY 177 KGTSPVAVANAVNCAETVYDILMDALTKANLMTDPLPCHFTSAFAGFCCTVYASPV 236

D6 180 KGLTPIMKINAVNCAEVVYDILERKLDYHLILDNPCCHFTSAFAGFCATVYASPV 239

QY 237 VVKTIRYNSALGOYSAGHCALTMLOKEGPRAFFYG 272

D6 240 VVKTIRYNSPPGOYSPDLDMIKVWAGGSPNAFFYG 275

RESULT 14
ITS-09-823

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Sequence 6, Application US/099232866A
Publication No. US20030150022A1
GENERAL INFORMATION:
APPLICANT: Newell, Martha
APPLICANT: Berry-Lowe, Sandra
TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
FILE REFERENCE: C1102/7902
CURRENT APPLICATION NUMBER: US/09/823,886A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,533
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ. ID NOS.: 16
SOFTWARE: PatentIn version 3.0
SEQ. ID NO. 6
LENGTH: 284
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-886A-6

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Query Match	63.4%;	Score 998.5;	DB 12;	Length 284;
Best Local Similarity	71.0%;	Pred. No. 1.7e-96;		
Matches 196;	Conservative 30;	Mismatches 45;	Indels 5;	Gaps 3;

Qy MVEFKETDVEPFAIVFELGAGTAACIADILEPPLTAYRQLQIGESQGPVRAIASQYR 60

Db MVLKRSDVPEPTNAVKFELGAGTAACFADLVTFPEPTAYRQLQIGENQA-QOTARLYQYR 68

Qy GWNQGLITLTVAREGPGSLYNGVADLQOMSPASVRIQLYDSVQFYT-KOSEHASIGSR 119

Db GVLGTLITLTVAREGPGSPENGLVADLQOMSPASIRQLYDSVQFYTPKQADNSLITLR 128

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Db 129 ILMGCTTGAAATCAQPDIVAKYRQASIHLDSPKSDKSGCTMDAKRTTAREGVAQGLW 188

Qy 177 KGSFNVAAKALVNCALVETVYDILIDALIKANLMTDILPCFTSAFAGPCTTYIAAPVD 233

Db 189 KGLPILPKIKRALVNCALVETVYDILEKLLDTHLLDNPFCFNVSAFGAGCAIVASAVD 248

Qy VVTRRYNSALGOYSAGHCALTMLQKQEPRAFYKG 272

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RESULT 15

US-09-823-886A-2
Sequence 2, Application US/09823886A
Publication No. US2003015002A1
GENERAL INFORMATION:
APPLICANT: Newell, Martha
APPLICANT: Berry-Lowe, Sandra
TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
FILE REFERENCE: C1102/77002
CURRENT APPLICATION NUMBER: US/09/823,886A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,533

; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 307
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-823-886A-2

Query Match 58.1%; Score 915; DB 12; Length 307;
 Best Local Similarity 59.3%; Pred. No. 1.2e-87;
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Qy	61	GVNGTILTMVRTGPRSLYNGLVAGLQKQSPASVRIGLYDSVKQFYTKSEHA-SIGSR	119
Db	57	GVIGTITAVVKTGSRMKLYSGLPAGLQKQISSASLRIGLYDTVGEFLTAGKETAPSLGSK	116
Qy	120	LLAGSTGALAVVAQPTDVYKRFQQAQARAGGR-RYOSTVNAKXTIAREDFRGLMKG	178
Db	117	ILAGLTGAVAVFPGQTEVYKVRLOAQSHLHGIXKPRYGTYNARILATTEGLTGLMKG	176
Qy	179	TSPVAFANATVNCALVTYDLIKDALIKANLMTDLPCHFTSAFGAGFCTTVIASPVDV	238
Db	177	TTPPLMRSVLINCELTETVYDLMKELAVKNNILADVPCHLVSAALLAGFCATMSSPVDV	236
Qy	239	KTRYMNSALQYSSAGHCALTMLOKEGPRAFYKGFMSFLRLGSNNVVMFTYEOLKRAL	298
Db	237	KTRFINSPPGQYKSPVPCAMKVFTEGPTAFKGLVPSFLRLGSNNVIMFVCFEOLKREL	296

Search completed: February 4, 2004, 09:24:59
 Job time : 35 secs.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 09:18:04 ; Search time 175 Seconds

(without alignments)
1606.657 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576
Sequence: 1 MWGFKATDVPPATVVKFLGA.....TYEOLKRALMAACTSRAPF 309Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:*

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32: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1576	100.0	309	PCT-US03-00253-132 Sequence 132, App

2	1576	100.0	309	1	PCT-US99-01198-1	Sequence 1, Appl
3	1576	100.0	309	1	PCT-US99-06311-3	Sequence 3, Appl
4	1576	100.0	309	1	PCT-US99-17246-2	Sequence 2, Appl
5	1576	100.0	309	14	US-09-012-218-1	Sequence 1, Appl
6	1576	100.0	309	15	US-09-124-293-2	Sequence 2, Appl
7	1576	100.0	309	16	US-09-277-575-8	Sequence 8, Appl
8	1576	100.0	309	17	US-09-353-645-1	Sequence 1, Appl
9	1576	100.0	309	18	US-09-433-622-34	Sequence 34, Appl
10	1576	100.0	309	19	US-09-599-760-4	Sequence 4, Appl
11	1576	100.0	309	21	US-09-711-022-8	Sequence 8, Appl
12	1576	100.0	309	21	US-09-711-022A-8	Sequence 8, Appl
13	1576	100.0	309	21	US-09-743-847-4	Sequence 4, Appl
14	1576	100.0	309	23	US-09-884-814-1	Sequence 1, Appl
15	1576	100.0	309	28	US-10-265-689-1	Sequence 1, Appl
16	1576	100.0	309	28	US-10-270-861-34	Sequence 34, Appl
17	1576	100.0	309	29	US-10-336-472-132	Sequence 132, App
18	1576	100.0	309	31	US-10-631-467-884	Sequence 884, App
19	1576	100.0	309	32	US-60-453-050-13010	Sequence 13010, A
20	1576	100.0	309	32	US-60-453-135-13010	Sequence 13010, A
21	1576	100.0	309	32	US-60-455-444-6960	Sequence 6960, Ap
22	1576	100.0	309	32	US-60-465-241-6960	Sequence 6960, Ap
23	1576	100.0	309	32	US-60-466-412-13010	Sequence 13010, A
24	1576	100.0	314	23	US-09-823-886A-4	Sequence 4, Appl
25	1576	100.0	337	24	US-09-949-016-9410	Sequence 9410, Ap
26	1572	99.7	309	1	PCT-US99-01198-3	Sequence 3, Appl
27	1572	99.7	309	1	PCT-US99-12623-4	Sequence 4, Appl
28	1572	99.7	309	1	PCT-US99-17246-6	Sequence 6, Appl
29	1572	99.7	309	8	US-08-470-868-51	Sequence 51, Appl
30	1572	99.7	309	9	US-08-518-878A-51	Sequence 51, Appl
31	1572	99.7	309	12	US-08-807-861-51	Sequence 51, Appl
32	1572	99.7	309	12	US-08-946-719-51	Sequence 51, Appl
33	1572	99.7	309	14	US-09-012-218-3	Sequence 3, Appl
34	1572	99.7	309	14	US-09-093-662-4	Sequence 4, Appl
35	1572	99.7	309	15	US-09-124-293-6	Sequence 6, Appl
36	1572	99.7	309	17	US-09-397-342-17	Sequence 17, Appl
37	1572	99.7	309	17	US-09-397-342A-17	Sequence 17, Appl
38	1572	99.7	309	23	US-09-597-342C-17	Sequence 17, Appl
39	1572	99.7	309	23	US-09-884-814-6	Sequence 6, Appl
40	1570	99.6	309	1	PCT-US99-01198-2	Sequence 2, Appl
41	1570	99.6	309	1	PCT-US99-17246-8	Sequence 8, Appl
42	1570	99.6	309	14	US-09-012-218-2	Sequence 2, Appl
43	1570	99.6	309	14	US-09-124-293-8	Sequence 8, Appl
44	1570	99.6	309	23	US-09-884-814-8	Sequence 8, Appl
45	1570	99.6	309	26	US-10-001-051B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
PCT-US03-00253-132
Sequence 132, Application PC/TUS0300253
GENERAL INFORMATION:
APPLICANT: Carigen Corp. et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-533C-061 (CURA 833C WO)
CURRENT APPLICATION NUMBER: PCT/US03/00253
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: 10/336,472
PRIOR FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 10/080,334
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/092,900
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 10/136,826
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 10/236,417
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/345,092
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/345,219
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/348,804

; PRIOR FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: 60/349,182
 ; PRIOR FILING DATE: 2002-01-16
 ; PRIOR APPLICATION NUMBER: 60/349,733
 ; PRIOR FILING DATE: 2002-01-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: Cuiaseq1st version 0.1
 ; SEQ ID NO 132
 ; LENGTH: 309
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PCT-US03-00253-132

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 Best Local Similarity 100.0%; Pred. No. 1.8e-159;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 181 PNVARNALVNCALVTVYDILKDALIKANLMTDDLPCHTSAFAGFCTTVIASPVDVYKT 240
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 DB 241 RYMNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
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 DB 301 ACTSREAPF 309

RESULT 2
 PCT-US99-01198-1
 ; Sequence 1, Application PC/TUS9901198
 ; GENERAL INFORMATION:
 ; APPLICANT: Picoult-Vrolijk, Leslie
 ; TITLE OF INVENTION: Single Nucleotide Polymorphisms of the
 ; FILE REFERENCE: 04990.0048
 ; CURRENT APPLICATION NUMBER: PCT/US99/01198
 ; EARLIER FILING DATE: 1999-01-21
 ; EARLIER APPLICATION NUMBER: 09/012,21
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 309
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PCT-US99-01198-1

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 DB 1 MGGFKATDVPPATATVKEFGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 QY 61 GVMGTLTMVTEGPRSLVNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
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RESULT 3
 PCT-US99-06317-3
 ; Sequence 3, Application PC/TUS9906317
 ; GENERAL INFORMATION:
 ; APPLICANT: Garvey, W. Timothy
 ; APPLICANT: Argyropoulos, George
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING A RISK TO UCP2 AND UCP3
 ; TITLE OF INVENTION: GENE VARIANT-RELATED AFFILIATIONS AND COMPOSITIONS
 ; FILE REFERENCE: 19113.0069/P
 ; CURRENT APPLICATION NUMBER: PCT/US99/06317
 ; CURRENT FILING DATE: 1999-03-23
 ; EARLIER APPLICATION NUMBER: 60/078,972
 ; EARLIER FILING DATE: 1998-03-23
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 309
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; OTHER INFORMATION: Note:/corresponds to human UCP2
 ; PCT-US99-06317-3

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RESULT 4


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RESULT 7
US-09-277-575-8
; Sequence 8, Application US/09277575
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha K.
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO
; FILE OF INVENTION: METABOLIC INTERACTIONS IN DISEASE
; FILE REFERENCE: V0139/7028/HK
; CURRENT APPLICATION NUMBER: US/09/277,575
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: U.S. 60/082,250
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: U.S. 60/094,519
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: U.S. 60/101,580
; EARLIER FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 13
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; SEQ ID NO 8
; LENGTH: 309
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; ORGANISM: Homo Sapiens
US-09-277-575-8

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Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 PNVARNAIVNCALVELTYDILKDALIKANLMTDDLPCHTSAFGAGCTTIVIASPVDVYKT 240
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DB 301 ACTSREAPF 309

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RESULT 8
US-09-353-645-1
; Sequence 1, Application US/09353645
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICOUTIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/09/353,645
; CURRENT FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 309
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; ORGANISM: Homo sapiens
US-09-353-645-1

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Best Local Similarity 100.0%; Pred. No. 1.8e-159;
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DB 301 ACTSREAPF 309

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RESULT 9
US-09-433-622-34
; Sequence 34, Application US/09433622A
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Adams, Sean
; TITLE OF INVENTION: UCPS
; FILE REFERENCE: P1663R2
; CURRENT APPLICATION NUMBER: US/09/433,622A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: US 60/110,286
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: US 60/129,583
; EARLIER FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: US 60/143,886
; EARLIER FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 34
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-433-622-34

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Query Match          100.0%; Score 1576; DB 18; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGFKATDVPTATVKEFGAGTACIADLITFPDITAKVRLQIGESQGPVATASAOYR 60
DB 1 MGFKATDVPTATVKEFGAGTACIADLITFPDITAKVRLQIGESQGPVATASAOYR 60
QY 61 GWMGTTILMTVTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTTILMTVTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAVAAVAPPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAVAPPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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QY      181 PNVARNAINVCAELVYDILIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
      |||||
Db      181 PNVARNAINVCAELVYDILIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240

QY      241 RYNNNSALGOYSSAGHCALTMLOKESGPRAFYKGMPSFELGSMNVMMFVYEQLRALMA 300
      |||||
Db      241 RYNNNSALGOYSSAGHCALTMLOKESGPRAFYKGMPSFELGSMNVMMFVYEQLRALMA 300

QY      301 ACTSREAPF 309
      |||||
Db      301 ACTSREAPF 309

```

```

RESULT 10
US-09-599-760-4
; Sequence 4, Application US/09599760
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha K.
; TITLE OF INVENTION: Methods and Products for Manipulating
; TITLE OF INVENTION: Uncoupling Protein Expression in the Plasma Membrane
; FILE REFERENCE: 10277/7009
; CURRENT APPLICATION NUMBER: US/09/599,760
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/140,574
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-599-760-4

```

```

Query Match      100.0%; Score 1576; DB 19; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MNGFKATDVPPATATVFKFLGAGTAACTADLITPPLDTAKVRLQIQESGQPVATASQYR 60
      |||||
Db      1 MNGFKATDVPPATATVFKFLGAGTAACTADLITPPLDTAKVRLQIQESGQPVATASQYR 60

QY      61 GVMGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
      |||||
Db      61 GVMGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFTYKSGEHSISGRL 120

QY      121 LAGSTGALAAVAAPPTDVVKVRFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
      |||||
Db      121 LAGSTGALAAVAAPPTDVVKVRFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180

QY      181 PNVARNAINVCAELVYDILIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
      |||||
Db      181 PNVARNAINVCAELVYDILIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240

QY      241 RYNNNSALGOYSSAGHCALTMLOKESGPRAFYKGMPSFELGSMNVMMFVYEQLRALMA 300
      |||||
Db      241 RYNNNSALGOYSSAGHCALTMLOKESGPRAFYKGMPSFELGSMNVMMFVYEQLRALMA 300

QY      301 ACTSREAPF 309
      |||||
Db      301 ACTSREAPF 309

```

```

RESULT 11
US-09-711-022-8
; Sequence 8, Application US/09711022
; GENERAL INFORMATION:
; APPLICANT: MARTHA K. NEWELL
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO
; TITLE OF INVENTION: METABOLIC INTERACTIONS IN DISEASE
; FILE REFERENCE: V0139/7028
; CURRENT APPLICATION NUMBER: US/09/711,022
; CURRENT FILING DATE: 2000-11-09

```

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; PRIOR APPLICATION NUMBER: U.S. 60/082,250
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: U.S. 60/094,519
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: U.S. 60/101,580
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-711-022-8

```

```

Query Match      100.0%; Score 1576; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MNGFKATDVPPATATVFKFLGAGTAACTADLITPPLDTAKVRLQIQESGQPVATASQYR 60
      |||||
Db      1 MNGFKATDVPPATATVFKFLGAGTAACTADLITPPLDTAKVRLQIQESGQPVATASQYR 60

QY      61 GVMGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
      |||||
Db      61 GVMGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFTYKSGEHSISGRL 120

QY      121 LAGSTGALAAVAAPPTDVVKVRFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
      |||||
Db      121 LAGSTGALAAVAAPPTDVVKVRFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180

QY      181 PNVARNAINVCAELVYDILIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
      |||||
Db      181 PNVARNAINVCAELVYDILIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240

QY      241 RYNNNSALGOYSSAGHCALTMLOKESGPRAFYKGMPSFELGSMNVMMFVYEQLRALMA 300
      |||||
Db      241 RYNNNSALGOYSSAGHCALTMLOKESGPRAFYKGMPSFELGSMNVMMFVYEQLRALMA 300

QY      301 ACTSREAPF 309
      |||||
Db      301 ACTSREAPF 309

```

```

RESULT 12
US-09-711-022A-8
; Sequence 8, Application US/09711022A
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha K
; TITLE OF INVENTION: Methods and products related to metabolic interactions in di
; FILE REFERENCE: V0139/7028
; CURRENT APPLICATION NUMBER: US/09/711,022A
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/094,519
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: US 60/101,580
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-711-022A-8

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```

Query Match      100.0%; Score 1576; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MNGFKATDVPPATATVFKFLGAGTAACTADLITPPLDTAKVRLQIQESGQPVATASQYR 60
      |||||
Db      1 MNGFKATDVPPATATVFKFLGAGTAACTADLITPPLDTAKVRLQIQESGQPVATASQYR 60

QY      61 GVMGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
      |||||

```

```

Db      61 GWMGTLTMVTEGPRSLYNGLVAGLQOMSFASVRLGLDYSVQFPTKSEHASIGSRL 120
Qy      121 LAGSTTGALAAVAAPPTDVVKRFPQAQARAGGRRYOSTVNAKTIAREEGFGLMKGS 180
Db      121 LAGSTTGALAAVAAPPTDVVKRFPQAQARAGGRRYOSTVNAKTIAREEGFGLMKGS 180
Qy      181 PNVARNALVNCALVLYDILKDALIKALMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
Db      181 PNVARNALVNCALVLYDILKDALIKALMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
Qy      241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVMFVTEQLKRALMA 300
Db      241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVMFVTEQLKRALMA 300
Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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RESULT 13
US-09-743-847-4
; Sequence 4, Application US/09743847
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108 .0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-847-4

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```

Query Match      100.0%; Score 1576; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MNGFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGESQGPVATASAOYR 60
Db      1 MNGFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGESQGPVATASAOYR 60
Qy      61 GWMGTLTMVTEGPRSLYNGLVAGLQOMSFASVRLGLDYSVQFPTKSEHASIGSRL 120
Db      61 GWMGTLTMVTEGPRSLYNGLVAGLQOMSFASVRLGLDYSVQFPTKSEHASIGSRL 120
Qy      121 LAGSTTGALAAVAAPPTDVVKRFPQAQARAGGRRYOSTVNAKTIAREEGFGLMKGS 180
Db      121 LAGSTTGALAAVAAPPTDVVKRFPQAQARAGGRRYOSTVNAKTIAREEGFGLMKGS 180
Qy      181 PNVARNALVNCALVLYDILKDALIKALMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
Db      181 PNVARNALVNCALVLYDILKDALIKALMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
Qy      241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVMFVTEQLKRALMA 300
Db      241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVMFVTEQLKRALMA 300
Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

```

```

RESULT 14
US-09-884-814-1
; Sequence 1, Application US/09884814
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, W. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; FILE REFERENCE: 018781-001110US
; CURRENT APPLICATION NUMBER: US/09/884,814
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
; US-09-884-814-1

```

```

Query Match      100.0%; Score 1576; DB 23; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 MNGFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGESQGPVATASAOYR 60
Db      1 MNGFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGESQGPVATASAOYR 60
Qy      61 GWMGTLTMVTEGPRSLYNGLVAGLQOMSFASVRLGLDYSVQFPTKSEHASIGSRL 120
Db      61 GWMGTLTMVTEGPRSLYNGLVAGLQOMSFASVRLGLDYSVQFPTKSEHASIGSRL 120
Qy      121 LAGSTTGALAAVAAPPTDVVKRFPQAQARAGGRRYOSTVNAKTIAREEGFGLMKGS 180
Db      121 LAGSTTGALAAVAAPPTDVVKRFPQAQARAGGRRYOSTVNAKTIAREEGFGLMKGS 180
Qy      181 PNVARNALVNCALVLYDILKDALIKALMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
Db      181 PNVARNALVNCALVLYDILKDALIKALMTDDLPCHTSAFGAGFCTTVIASPVVYKT 240
Qy      241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVMFVTEQLKRALMA 300
Db      241 RYMNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVMFVTEQLKRALMA 300
Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

```

```

RESULT 15
US-10-265-689-1
; Sequence 1, Application US/10265689
; GENERAL INFORMATION:
; APPLICANT: SURMITT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOUTILAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15

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NUMBER OF SEQ ID NOS: 47
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 1
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-265-689-1

Query Match 100.0%; Score 1576; DB 28; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1,8e-159;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVGFKATDVPPPTATVTKFLGAGTACTADLITFPPLDTAKVRLQIQESQGPVATASQYR	60
DB	1	MVGFKATDVPPPTATVTKFLGAGTACTADLITFPPLDTAKVRLQIQESQGPVATASQYR	60
QY	61	GVNGTILTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYTKGSEHASIGSRL	120
DB	61	GVNGTILTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYTKGSEHASIGSRL	120
QY	121	LASSTGALAVAAQPTDVVKVRFQQAQARAGGRYQSTVNAKYTIAREEGFRGLMKGTS	180
DB	121	LASSTGALAVAAQPTDVVKVRFQQAQARAGGRYQSTVNAKYTIAREEGFRGLMKGTS	180
QY	181	PNVARNALVNCALVTVYDILKDALKANLMTDDLPGHFTSAFGAGFCTVIASPDVVKYI	240
DB	181	PNVARNALVNCALVTVYDILKDALKANLMTDDLPGHFTSAFGAGFCTVIASPDVVKYI	240
QY	241	RYNNSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRIGSNVVMFVTTYEQLKALMA	300
DB	241	RYNNSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRIGSNVVMFVTTYEQLKALMA	300
QY	301	ACTSREAPF 309	
DB	301	ACTSREAPF 309	

Search completed: February 4, 2004, 09:23:37
 Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:18:34 ; Search time 23 Seconds
(without alignments)
1045.650 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576

Sequence: 1 MGFKATDVPPTATVKFLGA.....TYEQKRALMAACTSRAPF 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 376054 seqs, 77831530 residues

Total number of hits satisfying chosen parameters: 376054

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_AA.New.*
1: /cgm2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgm2_6/prodata/1/paa/US06_NEW_COMB.pep.*
3: /cgm2_6/prodata/1/paa/US07_NEW_COMB.pep.*
4: /cgm2_6/prodata/1/paa/US08_NEW_COMB.pep.*
5: /cgm2_6/prodata/1/paa/US09_NEW_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1576	100.0	309	5	US-09-599-760B-4
2	1576	100.0	309	6	US-10-671-628-8
3	1576	100.0	309	6	US-10-616-865-8
4	1576	100.0	309	7	US-60-485-450-1467
5	1496	94.9	309	6	US-10-743-643-170
6	1496	94.9	309	7	US-60-531-341-501
7	1149.5	72.9	312	6	US-10-671-628-9
8	1149.5	72.9	312	7	US-60-490-890-852
9	998.5	63.4	275	5	US-09-599-760B-6
10	998.5	63.4	275	6	US-10-616-865-10
11	998.5	63.4	275	6	US-10-743-643-172
12	998.5	63.4	275	7	US-60-490-890-854
13	998.5	63.4	275	7	US-60-531-341-503
14	915	58.1	307	5	US-09-599-760B-2
15	915	58.1	307	6	US-10-616-865-6
16	907	57.6	307	6	US-10-671-628-7
17	693	44.0	345	6	US-10-425-114A-66317
18	674.5	42.8	303	6	US-10-671-628-2
19	671.5	42.6	306	6	US-10-671-628-5
20	663.5	42.1	314	6	US-10-671-628-6
21	594	37.7	348	6	US-10-671-628-4
22	495	31.4	300	5	US-09-614-150A-14019
23	492.5	31.2	341	6	US-10-425-114A-52234
24	479.5	30.4	303	5	US-09-614-150A-16338
25	455.5	28.9	330	6	US-10-739-830-6246
26	441.5	28.0	336	1	PCT-US03-28227-4124

27	436.5	27.7	329	6	US-10-258-899A-1936	Sequence 1936, Ap
28	420.5	26.7	337	5	US-09-614-150A-27447	Sequence 27447, A
29	416.5	26.4	314	6	US-10-743-643-1602	Sequence 1602, Ap
30	416.5	26.4	314	7	US-60-531-341-1432	Sequence 1432, Ap
31	411.5	26.1	314	6	US-10-743-643-1604	Sequence 1604, Ap
32	411.5	26.1	314	7	US-60-531-341-1434	Sequence 1434, Ap
33	408	25.9	312	6	US-10-425-114A-59754	Sequence 59754, A
34	408	25.9	335	5	US-09-614-150A-19419	Sequence 19419, A
35	403	25.6	335	6	US-10-432-737-5	Sequence 5, Appl
36	400	25.4	317	5	US-09-614-150A-815	Sequence 816, Appl
37	389	24.7	311	5	US-09-614-150A-27690	Sequence 27690, A
38	387.5	24.6	342	1	PCT-US03-24164-45	Sequence 45, Appl
39	370	23.5	280	5	US-09-614-150A-24396	Sequence 24396, A
40	370	23.5	280	5	US-09-614-150A-41871	Sequence 41871, A
41	367.5	23.3	301	5	US-09-614-150A-555	Sequence 555, App
42	360.5	22.9	287	5	US-09-614-150A-23403	Sequence 23403, A
43	349	22.1	296	5	US-09-614-150A-8460	Sequence 8460, Ap
44	345	21.9	302	5	US-09-614-150A-27507	Sequence 27507, A
45	340	21.6	263	1	PCT-US03-24164-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-599-760B-4
Sequence 4, Application US/09599760B
GENERAL INFORMATION:
APPLICANT: Newell, Marsha K
TITLE OF INVENTION: Methods and products for manipulating uncoupling protein
FILE REFERENCE: V00135, 70059, US
CURRENT APPLICATION NUMBER: US/09/599, 760B
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/140, 574
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-599-760B-4

Query Match	100.0%;	Score 1576;	DB 5;	Length 309;
Best Local Similarity	100.0%;	Pred. No. 2.6e-150;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGFKATDVPPTATVKFLGAGTAACTADLTFFPDTAKVRLQIQESQGPVATASAOYR	60	
DB	1	MGFKATDVPPTATVKFLGAGTAACTADLTFFPDTAKVRLQIQESQGPVATASAOYR	60	
QY	61	GWGCTILTWREGRSLYNGVLVAGLQVMSFASVRLGYSVQFTKSEHASTSRL	120	
DB	61	GWGCTILTWREGRSLYNGVLVAGLQVMSFASVRLGYSVQFTKSEHASTSRL	120	
QY	121	LAGSTGALAVVAQPTVVVVFQQAQAGGRYOSTVNAVYKTIARESEFRLMKTGS	180	
DB	121	LAGSTGALAVVAQPTVVVVFQQAQAGGRYOSTVNAVYKTIARESEFRLMKTGS	180	
QY	181	PVAVARNAVNCALVETTYDILIDALIKANIMTDDLPCHTTSFAGAGFCTTYIASVVDVKT	240	
DB	181	PVAVARNAVNCALVETTYDILIDALIKANIMTDDLPCHTTSFAGAGFCTTYIASVVDVKT	240	
QY	241	RYVNSALGVSSAGHCATMLQKGFRAFYKGFPSFRLSGNAVVMVETYEQLRALMA	300	
DB	241	RYVNSALGVSSAGHCATMLQKGFRAFYKGFPSFRLSGNAVVMVETYEQLRALMA	300	
QY	301	ACTSRAPF 309		
DB	301	ACTSRAPF 309		


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RESULT 2
US-10-671-628-8
; Sequence 8, Application US/10671628
; GENERAL INFORMATION:
; APPLICANT: ITO, Kikutsu
; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
; FILE REFERENCE: 2003-13864/MWC/00553
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/10/0671.628
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: PCT/JP00/03806
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: JP11-167439
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-628-8

Query Match      100.0%; Score 1576; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDTAKVRLQIQESQGPVATASAYR 60
DB 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDTAKVRLQIQESQGPVATASAYR 60
QY 61 GWMGTLTMTWRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLTMTWRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVVKRFQQAARAGGRRYQSTVNAKYKTIAREBGRGLMKGT 180
DB 121 LAGSTTGALAAVAAPPTDVVKRFQQAARAGGRRYQSTVNAKYKTIAREBGRGLMKGT 180
QY 181 PNVARNAIIVNCALVETVYDLIKDALIKANIMTDDLPCHTSAFGAGCTTVIASPVDVKT 240
DB 181 PNVARNAIIVNCALVETVYDLIKDALIKANIMTDDLPCHTSAFGAGCTTVIASPVDVKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 3
US-10-616-865-8
; Sequence 8, Application US/10616865
; GENERAL INFORMATION:
; APPLICANT: NEMELL, MARTHA K
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASE
; FILE REFERENCE: VO139.7001US0
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 09/277,575
; PRIOR FILING DATE: 1999-03-27
; PRIOR APPLICATION NUMBER: US 60/082,250
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/101,580
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/094,519
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 8
; LENGTH: 309

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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-865-8

Query Match      100.0%; Score 1576; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDTAKVRLQIQESQGPVATASAYR 60
DB 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDTAKVRLQIQESQGPVATASAYR 60
QY 61 GWMGTLTMTWRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLTMTWRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVVKRFQQAARAGGRRYQSTVNAKYKTIAREBGRGLMKGT 180
DB 121 LAGSTTGALAAVAAPPTDVVKRFQQAARAGGRRYQSTVNAKYKTIAREBGRGLMKGT 180
QY 181 PNVARNAIIVNCALVETVYDLIKDALIKANIMTDDLPCHTSAFGAGCTTVIASPVDVKT 240
DB 181 PNVARNAIIVNCALVETVYDLIKDALIKANIMTDDLPCHTSAFGAGCTTVIASPVDVKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

```

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RESULT 4
US-60-485-450-1467
; Sequence 1467, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CHANG, Sheng-xing
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: C1001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1467
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1467

Query Match      100.0%; Score 1576; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDTAKVRLQIQESQGPVATASAYR 60
DB 1 MNGFKATDVPPPTATVKEFLGAGTACIADLITPPLDTAKVRLQIQESQGPVATASAYR 60
QY 61 GWMGTLTMTWRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLTMTWRTGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPPTDVVKRFQQAARAGGRRYQSTVNAKYKTIAREBGRGLMKGT 180
DB 121 LAGSTTGALAAVAAPPTDVVKRFQQAARAGGRRYQSTVNAKYKTIAREBGRGLMKGT 180
QY 181 PNVARNAIIVNCALVETVYDLIKDALIKANIMTDDLPCHTSAFGAGCTTVIASPVDVKT 240
DB 181 PNVARNAIIVNCALVETVYDLIKDALIKANIMTDDLPCHTSAFGAGCTTVIASPVDVKT 240

```


QY 120 LLAGSTTGALAAVAAQPTDVVKVTFQQAQABAG--GGRYQSTVNAKYTLAEEGRGLW 176
 DB 120 ILAAGTTGAAAVTCAQPTDVVKVTFQQAQABAG--GGRYQSTVNAKYTLAEEGRGLW 179
 QY 177 KGTSPNVAARNAIYVCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVIAASPD 236
 DB 180 KGTLPNIMRNALIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVIAASPD 239
 QY 237 VKTRRYNSALGOYSSAGHCALTMLOKEGPRAFYKGMBSFRLGSMVVMFTYEQLR 296
 DB 240 VKTRRYNSPPGOYFSPDLDCMIKVAQEGPTAFYKGMBSFRLGSMVVMFTYEQLR 299
 QY 297 ALMAACTSREAPF 309
 DB 300 ALMKVQMLRESPF 312

RESULT 8
 US-60-490-890-852
 ; Sequence 852, Application US/60490890
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Martha
 ; APPLICANT: Kuprow, Brent A.
 ; APPLICANT: Webster, Kevin R.
 ; APPLICANT: Jackson, Donald
 ; APPLICANT: Wong, Tai W.
 ; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
 ; FILE REFERENCE: D03:0 PSP
 ; CURRENT APPLICATION NUMBER: US/60-490,890
 ; NUMBER OF SEQ ID NOS: 2779
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 852
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-490-890-852

Query Match 72.9%; Score 1149.5; DB 7; Length 312;
 Best Local Similarity 72.2%; Pred. No. 1.9e-107;
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MGGFKATDVPPATATVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 60
 DB 1 MGLKPSDVPPTMAVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 59
 QY 61 GVGGITLTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
 DB 60 GVLGITLTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYTPKGDNSLITTR 119
 QY 120 LLAGSTTGALAAVAAQPTDVVKVTFQQAQABAG--GGRYQSTVNAKYTLAEEGRGLW 176
 DB 120 ILAAGTTGAAAVTCAQPTDVVKVTFQQAQABAG--GGRYQSTVNAKYTLAEEGRGLW 179
 QY 177 KGTSPNVAARNAIYVCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVIAASPD 236
 DB 180 KGTLPNIMRNALIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVIAASPD 239
 QY 237 VKTRRYNSALGOYSSAGHCALTMLOKEGPRAFYKGMBSFRLGSMVVMFTYEQLR 296
 DB 240 VKTRRYNSPPGOYFSPDLDCMIKVAQEGPTAFYKGMBSFRLGSMVVMFTYEQLR 299
 QY 297 ALMAACTSREAPF 309
 DB 300 ALMKVQMLRESPF 312

RESULT 9
 US-09-599-760B-6
 ; Sequence 6, Application US/09599760B
 ; GENERAL INFORMATION:
 ; APPLICANT: Newell, Martha K
 ; TITLE OF INVENTION: Methods and products for manipulating uncoupling protein

; TITLE OF INVENTION: expression
 ; FILE REFERENCE: Y00139, 70059, US
 ; CURRENT APPLICATION NUMBER: US/09/599, 760B
 ; CURRENT FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: US 60/140, 574
 ; PRIOR FILING DATE: 1999-06-23
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-599-760B-6

Query Match 63.4%; Score 998.5; DB 5; Length 275;
 Best Local Similarity 71.0%; Pred. No. 2.4e-92;
 Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY 1 MGGFKATDVPPATATVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 60
 DB 1 MGLKPSDVPPTMAVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 59
 QY 61 GVGGITLTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
 DB 60 GVLGITLTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYTPKGDNSLITTR 119
 QY 120 LLAGSTTGALAAVAAQPTDVVKVTFQQAQABAG--GGRYQSTVNAKYTLAEEGRGLW 176
 DB 120 ILAAGTTGAAAVTCAQPTDVVKVTFQQAQABAG--GGRYQSTVNAKYTLAEEGRGLW 179
 QY 177 KGTSPNVAARNAIYVCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVIAASPD 236
 DB 180 KGTLPNIMRNALIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVIAASPD 239
 QY 237 VKTRRYNSALGOYSSAGHCALTMLOKEGPRAFYKGMBSFRLGSMVVMFTYEQLR 296
 DB 240 VKTRRYNSPPGOYFSPDLDCMIKVAQEGPTAFYKGMBSFRLGSMVVMFTYEQLR 299

RESULT 10
 US-10-616-865-10
 ; Sequence 10, Application US/10616865
 ; GENERAL INFORMATION:
 ; APPLICANT: NEWELL, MARTHA K
 ; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN D
 ; FILE REFERENCE: Y0139, 70017US00
 ; CURRENT APPLICATION NUMBER: US/10/616, 865
 ; CURRENT FILING DATE: 2003-07-05
 ; PRIOR APPLICATION NUMBER: US 09/277, 575
 ; PRIOR FILING DATE: 1999-03-27
 ; PRIOR APPLICATION NUMBER: US 60/082, 250
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: US 60/101, 580
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: US 60/094, 519
 ; PRIOR FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 10
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-616-865-10

Query Match 63.4%; Score 998.5; DB 6; Length 275;
 Best Local Similarity 71.0%; Pred. No. 2.4e-92;
 Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY 1 MGGFKATDVPPATATVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 60
 DB 1 MGLKPSDVPPTMAVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 59
 QY 61 GVGGITLTMVTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119

```

Db      60 GVLGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      120 LLAGSTTGALAAVAAQPTDVVKVRFQAQARAG---GGRRYOSTVNAKYTIAREEGFGLW 176
      120 ILAGCTTGAAVAAVCAQPTDVVKVRFQASIHLPSPSDRKYSGMTDAYRTIAREEGVGLW 179
      177 KGTSPVNAANAIVNCAELVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVD 236
      180 KGTLPNIMENAIYNCAEVVYTDILKEKLDYHLITDNPCHFSVAFGAGFCATVVASPVD 239

QY      237 VVKTRYNSALQYSSAGHCALTMLOKEGPPAFYKG 272
      240 VVKTRYNSPPGQYFSPLDCKIMVAQEGPTAFYKG 275

RESULT 11
US-10-743-643-172
; Sequence 172, Application US/10743643
; GENERAL INFORMATION:
; APPLICANT: Woolf et al.
; TITLE OF INVENTION: Nucleic acid and amino acid sequences involved in pain
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/743,643
; PRIORITY FILING DATE: 2003-12-22
; FILE REFERENCE: 17633/2005
; PRIORITY FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 10/219,051
; PRIOR FILING DATE: 2002/07/14
; NUMBER OF SEQ ID NOS: 2605
; SOFTWARE: perl script
; SEQ ID NO 172
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Refseq / NP_073714
; DATABASE ENTRY DATE: 2001-03-09
US-10-743-643-172

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```

Query Match      63.4%; Score 998.5; DB 6; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY      1 MVEGKATDVPPATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESGQPVRAATASQYR 60
      1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQENQA-VQTAALVQYR 59
      61 GVMGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      60 GVLGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      120 LLAGSTTGALAAVAAQPTDVVKVRFQAQARAG---GGRRYOSTVNAKYTIAREEGFGLW 176
      120 ILAGCTTGAAVAAVCAQPTDVVKVRFQASIHLPSPSDRKYSGMTDAYRTIAREEGVGLW 179
      177 KGTSPVNAANAIVNCAELVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVD 236
      180 KGTLPNIMENAIYNCAEVVYTDILKEKLDYHLITDNPCHFSVAFGAGFCATVVASPVD 239

QY      237 VVKTRYNSALQYSSAGHCALTMLOKEGPPAFYKG 272
      240 VVKTRYNSPPGQYFSPLDCKIMVAQEGPTAFYKG 275

Db

```

```

RESULT 12
US-60-490-890-854
; Sequence 854, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION

```

```

; FILE REFERENCE: D0310 PSE
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 854
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-854

```

```

Query Match      63.4%; Score 998.5; DB 7; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY      1 MVEGKATDVPPATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESGQPVRAATASQYR 60
      1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQENQA-VQTAALVQYR 59
      61 GVMGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      60 GVLGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      120 LLAGSTTGALAAVAAQPTDVVKVRFQAQARAG---GGRRYOSTVNAKYTIAREEGFGLW 176
      120 ILAGCTTGAAVAAVCAQPTDVVKVRFQASIHLPSPSDRKYSGMTDAYRTIAREEGVGLW 179
      177 KGTSPVNAANAIVNCAELVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVD 236
      180 KGTLPNIMENAIYNCAEVVYTDILKEKLDYHLITDNPCHFSVAFGAGFCATVVASPVD 239

QY      237 VVKTRYNSALQYSSAGHCALTMLOKEGPPAFYKG 272
      240 VVKTRYNSPPGQYFSPLDCKIMVAQEGPTAFYKG 275

Db

```

```

RESULT 13
US-60-531-341-503
; Sequence 503, Application US/60531341
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts Gene
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleic acid sequences involved in pain
; FILE REFERENCE: 17633/2041
; CURRENT APPLICATION NUMBER: US/60/531,341
; PRIORITY FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: perl script
; SEQ ID NO 503
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Refseq / NP_073714
; DATABASE ENTRY DATE: 2003-10-05
US-60-531-341-503

```

```

Query Match      63.4%; Score 998.5; DB 7; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY      1 MVEGKATDVPPATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESGQPVRAATASQYR 60
      1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQENQA-VQTAALVQYR 59
      61 GVMGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      60 GVLGTLITWRTGPGSPYNGVAGLQROMSPFASIRILYDSVKQVTPPKADNSLITR 119
      120 LLAGSTTGALAAVAAQPTDVVKVRFQAQARAG---GGRRYOSTVNAKYTIAREEGFGLW 176
      120 ILAGCTTGAAVAAVCAQPTDVVKVRFQASIHLPSPSDRKYSGMTDAYRTIAREEGVGLW 179

Db

```

```

QY 177 KGTSPNVAARNALVNCALVITYDLIKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPD 236
DB 180 KGTLPNIMRNALVNCALVITYDLIKDALIKANIMTDDLPCHFTSAGAGCAIVVAVSPD 239
QY 237 VKTRVNSALGOYSSAGHCAITMLQKEGPRAFYK 272
DB 240 VKTRVNSPPGOYFSPDCKMTKVAQEGPRAFYK 275

```

RESULT 14

```

US-09-599-760B-2
Sequence 2, Application US/09599760B
GENERAL INFORMATION:
APPLICANT: Newell, Martha K
TITLE OF INVENTION: Methods and products for manipulating uncoupling protein
FILE REFERENCE: V00139.70059.US
CURRENT APPLICATION NUMBER: US/09/599.760B
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/140,574
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 307
TYPE: PRT
ORGANISM: Homo sapiens
US-09-599-760B-2

```

Query Match 58.1%; Score 915; DB 5; Length 307;

Best Local Similarity 59.3%; Pred. No. 6,7e-84;

Matches 178; Conservative 48; Mismatches 68; Indels 6; Gaps 3;

```

QY 1 MGEFKATDVPPTATVFKFLAGTACIADITPPDPTAKVRLQIGESGQPVATASQYR 60
DB 1 MGGLTASDVHPTLGVQLFSAGIAACIADVITPPDPTAKVRLQVQGECP---TSSVIRYK 56
QY 61 GWMGTLITVWTEGPRSLYNGVAGLQROMSPASVRIGLYDSVKQFTYKGEHA-SIGSR 119
DB 57 GVLGTTAVVKTGKRMKLYSGLPAGLQRISSASLRIGLYDVQEFLLAGKETAPSLGSK 116
QY 120 LLAGSTTGALAVVAQPTDYKVRFOAQRAGGGR-RYOSTVNAKYTIAREGFRGLMKG 178
DB 117 ILAGLTGGVAVFIGQPTFVAVKRLQAQSHLHGKRYGTYNAYRIIATTEGLTGLMKG 176
QY 179 TSPNVAARNALVNCALVITYDLIKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPDV 238
DB 177 TTPNLMRSVLIINCTELVYDLMKEAFVKNIIADDPCHLVSALTAGFCATMSSPDVV 236
QY 239 KTRVNSALGOYSSAGHCAITMLQKEGPRAFYKGFNPFLRLGSMNVVWFYIEQLKRAL 298
DB 237 KTRFINSPPGOYKSVPCAMKVFTEGPTAFPKGLVPSFLRLGSMNVVWFVCFEQLKREL 296

```

RESULT 15

```

US-10-616-865-6
Sequence 6, Application US/10616865
GENERAL INFORMATION:
APPLICANT: NEWELL, MARTHA K
TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASE
FILE REFERENCE: V0139.70017US00
CURRENT APPLICATION NUMBER: US/10/616,865
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 09/277,575
PRIOR FILING DATE: 1999-03-27
PRIOR APPLICATION NUMBER: US 60/082,250
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/101,580
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 60/094,519
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2

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```

; SEQ ID NO 6
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-865-6

```

Query Match 58.1%; Score 915; DB 6; Length 307;

Best Local Similarity 59.3%; Pred. No. 6,7e-84;

Matches 178; Conservative 48; Mismatches 68; Indels 6; Gaps 3;

```

QY 1 MGEFKATDVPPTATVFKFLAGTACIADITPPDPTAKVRLQIGESGQPVATASQYR 60
DB 1 MGGLTASDVHPTLGVQLFSAGIAACIADVITPPDPTAKVRLQVQGECP---TSSVIRYK 56
QY 61 GWMGTLITVWTEGPRSLYNGVAGLQROMSPASVRIGLYDSVKQFTYKGEHA-SIGSR 119
DB 57 GVLGTTAVVKTGKRMKLYSGLPAGLQRISSASLRIGLYDVQEFLLAGKETAPSLGSK 116
QY 120 LLAGSTTGALAVVAQPTDYKVRFOAQRAGGGR-RYOSTVNAKYTIAREGFRGLMKG 178
DB 117 ILAGLTGGVAVFIGQPTFVAVKRLQAQSHLHGKRYGTYNAYRIIATTEGLTGLMKG 176
QY 179 TSPNVAARNALVNCALVITYDLIKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPDV 238
DB 177 TTPNLMRSVLIINCTELVYDLMKEAFVKNIIADDPCHLVSALTAGFCATMSSPDVV 236
QY 239 KTRVNSALGOYSSAGHCAITMLQKEGPRAFYKGFNPFLRLGSMNVVWFYIEQLKRAL 298
DB 237 KTRFINSPPGOYKSVPCAMKVFTEGPTAFPKGLVPSFLRLGSMNVVWFVCFEQLKREL 296

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Search completed: February 4, 2004, 09:24:12

Job time : 24 secs

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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:16:38 ; Search time 21 Seconds
(without alignments)

1415.053 Million cell updates/sec

Title: US-09-884-814-1
Perfect score: 1576
Sequence: 1 MVGFKATDVPPATVFKLGA.....TYEQKRALMACTSRAPF 309

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Match	Query Length	DB ID	Description
1	1149.5	72.9	312	2 JCS522	uncoupling protein
2	959.5	60.9	306	2 A52446	uncoupling protein
3	928.5	58.9	307	2 A26294	uncoupling protein
4	915.5	58.1	307	2 B34268	uncoupling protein
5	915	58.1	307	2 G01858	uncoupling protein
6	911.5	57.8	306	2 A31106	mitochondrial unco
7	907.5	57.6	288	2 S03603	uncoupling protein
8	693.5	44.0	306	2 T47570	uncoupling protein
9	684.5	43.4	306	2 T52024	uncoupling protein
10	671.5	42.6	306	2 T07793	uncoupling protein
11	520.5	33.0	325	2 JC7553	brain mitochondria
12	483.5	30.7	313	2 T05577	uncoupling protein
13	475.5	30.2	313	2 D84613	hypothetical prote
14	466	29.6	305	2 H86274	hypothetical prote
15	446.5	28.3	323	2 T35459	hypothetical prote
16	415.5	26.4	314	2 A36305	2-oxoglutarate/mal
17	413	26.1	282	2 T49628	probable dicarboxy
18	411.5	26.1	314	2 A56650	2-oxoglutarate car
19	398.5	25.3	343	2 T15253	hypothetical prote
20	379.5	24.1	290	2 S44091	oxoglutarate/malat
21	360	22.8	298	2 S51351	hypothetical prote
22	338.5	21.5	324	2 S25357	mitochondrial unco
23	307	19.5	302	2 S85042	2-oxoglutarate/mal
24	307	19.5	302	2 S85040	2-oxoglutarate/mal
25	297.5	18.9	331	2 T51899	probable 2-oxogluc
26	297.5	18.6	322	2 S57116	probable carrier p
27	292.5	17.6	297	2 T07405	oxoglutarate/malat
28	277.5	17.6	93	2 S16082	uncoupling protein
29	273	17.3	311	2 G01789	citrate transpor

30	273	17.3	311	2 A46595	tricarboxylate tra
31	263.5	16.7	309	2 T48156	hypothetical prote
32	260.5	16.5	352	2 T01729	mitochondrial solu
33	256.5	16.3	447	2 T00435	probable mitochond
34	255.5	16.2	298	2 B43646	ADP ATP carrier pr
35	255.5	16.2	302	2 T38879	probable mitochond
36	254.5	16.1	298	1 S03894	ADP ATP carrier pr
37	254.5	16.1	299	2 S44554	citrate transport
38	254.5	16.1	298	2 T09109	envelope protein L
39	253.5	16.1	298	1 XWBO	ADP ATP carrier pr
40	253	16.1	329	2 S48269	mitochondrial car
41	252.5	16.0	307	2 S54080	carrier protein YM
42	252.5	16.0	355	2 T09110	envelope protein L
43	252	16.0	339	2 A41677	ADP ATP carrier pr
44	249.5	15.8	702	2 T16533	hypothetical prote
45	247	15.7	320	2 T37603	probable oxaloacet

ALIGNMENTS

RESULT 1
JC5522
uncoupling protein UCP3, mitochondrial - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 21-Jan-2000
C:Accession: JC5522
R:Vidal-Puig, A.; Solanes, G.; Grujic, D.; Flier, J.S.; Lowell, B.B.
Biochem. Biophys. Res. Commun. 235, 79-82, 1997
A:Title: UCP3: An uncoupling protein homologue expressed preferentially and abundan
A:Reference number: JC5522, PMID:97339440, PMID:9196039
A:Accession: JC5522
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-312 <VID>
A:Cross-references: DDBJ:AF001787; NID:G2198812; PIND:AA051369.1; PID:G2198813
A:Experimental source: skeletal muscle
C:Comment: This protein is an inner mitochondrial membrane transporter which dissip
C:Genetics:
A:Gene: GDB:UCP3
A:Cross-references: GDB:6278985
C:Superfamily: ADP/ATP carrier protein, ADP/ATP carrier protein repeat homology
C:Keywords: mitochondrion
F:10-106/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F:113-207/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F:214-301/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 72.9%; Score 1149.5; DB 2; Length 312;

Best Local Similarity 72.4%; Pred. No. 2.6e-91; Mismatches 51; Indels 5; Gaps 3;

QY	1	MVGFKATDVPPATVFKELGAGTAACIADLIITFPLDTAKVRLQIQGSGQGPVATASAQYR	60
DB	1	MVGLKRSVDVPPMTAAVFKELGAGTAACFADLVITFPLDTAKVRLQIQGSEMDA-VQIARLVQYR	59
QY	61	GVNCTITLMTWRTEGSPSLNGLVAGIQRQMSRVSRLGYSVKQFYT-KGSEHMSIGSR	119
DB	60	GVNCTITLMTWRTEGSPSPNGLVAGIQRQMSRVSRLGYSVKQVYTPPKADNSSLITR	119
QY	120	ILAGSTTGALAAVVAOPTDVVKVRFQQAARAG--GGRRYQSTVNAVYKTIAREEGFGWL	176
DB	120	ILAGCTTGAAAVTCAQPTDVVKVRFQASIHIGPSRSDKYGSTMDAVRTIAREEGVGLW	179
QY	177	KGTSPNVAIVNCAELVYDIKALIKANIMDDLECHTSAFAAGFCTTVASPD	236
DB	177	KGTLPENIKRAIVNCAELVYDIKLEKLDIHLHDNFPCFVSAFPAAGFCATVVASPVD	236
QY	237	VVKTRVNSALGOYSSAGHCALTMQLKQGPRAFYKGFMSFRLGSMNVMTVEQLR	296
DB	240	VVKTRVNSSPGGYFSPDLDCMKTQMAVQEGPTAFYKGFPSFRLGSMNVMTVEQLR	299
QY	297	ALMAACTSRAPF	309

Db 300 ALMKVQMLRESBP 312

RESULT 2

A24446
uncoupling protein - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 18-Feb-2000
C/Accession: A32446
R/Balogh, A.G.; Ridley, R.G.; Patel, H.V.; Freeman, K.B.
Biochem. Biophys. Res. Commun. 161, 156-161, 1989
A/Title: Rabbit brown adipose tissue uncoupling protein mRNA: use of only one of two pol
A/Reference number: A32446; MUID:89273628; PMID:2730654
A/Accession: A32446
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-306 <BA>
A/Cross-references: GB:X14696
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: duplication; mitochondrion; transmembrane protein
F/10-103/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F/109-201/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F/208-295/Domain: ADP, ATP carrier protein repeat homology <ACPI>

Query Match 60.9%; Score 959.5; DB 2; Length 306;
Best Local Similarity 61.3%; Pred. No. 5.7e-75;
Matches 164; Conservative 48; Mismatches 63; Indels 5; Gaps 3;

QY 1 MYGKATDVPPTATVYKFLGAGTACIADITFPPLDTAKVRLQIQSGSQGPVATASQYR 60
Db 1 MYGTTTDPPTMGKIFISAGVACIADITFPPLDTAKVRLQIQSGSQGPVATASQYR 56
QY 61 GVMGTLTMVTEGPRSLVNGLVAGLQRMSPASVRIGLYDVSKOFTKSEHASICSL 120
Db 57 GVLGTTTLAKTEGPKLISGLPAGLQRIQISFASIRKILYDVTEFTSGEFTSLGSKI 116
QY 121 LAGSTGALAVAAQPTDVYKRFQQAARAGGR-RYOSTVNAKYTIAREGFRGLMKG 179
Db 117 SAGLTGGAVALFVGQTEVVKRLQAQSHLHGLKRYGTGNVAVRIATLSLTMKGT 176
QY 180 SRVAVNAIVNCAELVTVYLLIDALKANIMTDDPCHEFTSAFGAFCCTVYASPVYV 239
Db 177 TPVLENNVINCETELVYDLMKALVREIILADDVPCHLISALAGFTILLSPDVYK 236
QY 240 TRYNSALGOYSAGHCALTMLOKGPRAFYKGFPSFLRLGSMNVVVFYTYEQIKRL 298
Db 237 TRINSPQGVASVPCAMTMTKSGPTAFPGFVPSFLRLGSMNVVVFYTYEQIKELM 296

RESULT 3

A26294
uncoupling protein - rat
N/Alternate names: UCP
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Feb-2000
C/Accession: A26294; A29278; S03842; A61566
R/Bouillaud, F.; Weissenbach, J.; Ricquier, D.
J. Biol. Chem. 261, 1487-1490, 1986
A/Reference number: A26294; MUID:86111804; PMID:3753702
A/Accession: A26294
A/Molecule type: mRNA
A/Residues: 1-307 <BN>
A/Cross-references: GB:M1814; NID:9207556; PIDN:AA19671.1; PID:9207557
R/Ridley, R.G.; Patel, H.V.; Gerber, G.E.; Morton, R.C.; Freeman, K.B.
Nucleic Acids Res. 14, 4025-4035, 1986
A/Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoch
A/Reference number: A29278; MUID:86212540; PMID:3012461
A/Accession: A29278
A/Molecule type: mRNA
A/Residues: 1-307 <RI>
A/Cross-references: GB:X03894; GB:M5500; NID:957446; PIDN:CAA27531.1; PID:957447
R/Bouillaud, F.; Raimbault, S.; Ricquier, D.
Biochem. Biophys. Res. Commun. 157, 783-792, 1988

A/Title: The gene for rat uncoupling protein: complete sequence, structure of prime
A/Reference number: S03842; MUID:89076317; PMID:3202878
A/Accession: S03842
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-307 <BO>

A/Cross-references: EMBL:X12925; NID:957444; PIDN:CAA31392.1; PID:957445
R/Ridley, R.G.; Patel, H.V.; Partlett, C.L.D.; Olynyk, K.A.; Reichling, S.; Freeman,
Biochem. Biophys. Res. Commun. 161, 156-161, 1989
A/Title: Immunological detection of cDNA clones encoding the uncoupling protein of
A/Reference number: A61566; MUID:86188126; PMID:2421800
A/Accession: A61566
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 254-307 <RID>
A/Comment: The source of this protein was brown adipocyte mitochondria.
C/Genetics:
A/Introns: 42/3; 109/1; 176/1; 210/1; 270/2
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: duplication; mitochondrion; transmembrane protein
F/10-103/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F/209-296/Domain: ADP, ATP carrier protein repeat homology <ACPI>

Query Match 58.9%; Score 928.5; DB 2; Length 307;
Best Local Similarity 58.2%; Pred. No. 2.6e-72;
Matches 181; Conservative 52; Mismatches 67; Indels 11; Gaps 4;

QY 1 MYGKATDVPPTATVYKFLGAGTACIADITFPPLDTAKVRLQIQSGSQGPVATASQYR 60
Db 1 MYGTTTDPPTMGKIFISAGVACIADITFPPLDTAKVRLQIQSGSQGPVATASQYR 56
QY 61 GVMGTLTMVTEGPRSLVNGLVAGLQRMSPASVRIGLYDVSKOFTKSEHASICSL 119
Db 57 GVLGTTTLAKTEGPKLISGLPAGLQRIQISFASIRKILYDVTEFTSGEFTSLGSKI 116
QY 120 LAGSTGALAVAAQPTDVYKRFQQAARAGGR-RYOSTVNAKYTIAREGFRGLMKG 178
Db 117 SAGLTGGAVALFVGQTEVVKRLQAQSHLHGLKRYGTGNVAVRIATLSLTMKGT 176
QY 179 TSPVAVNAIVNCAELVTVYLLIDALKANIMTDDPCHEFTSAFGAFCCTVYASPVYV 238
Db 177 TPVLENNVINCETELVYDLMKALVREIILADDVPCHLISALAGFTILLSPDVYK 236
QY 239 KTRYNNSALGOYSAGHCALTMLOKGPRAFYKGFPSFLRLGSMNVVVFYTYEQIKRL 298
Db 237 KTRFNISLPQGVPSVPCAMTMTKSGPTAFPGFVPSFLRLGSMNVVVFYTYEQIKEL 296
QY 299 MAA-----CTS 304
Db 297 MKSROYVDCTT 307

RESULT 4

S34268
uncoupling protein, inner mitochondrial membrane, brown fat - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Feb-2000
C/Accession: S34268; A24363; S20294; S02427
R/Raimbault, S.; Prieto, S.; Rial, E.; Bouillaud, F.
submitted to the EMBL Data Library, June 1993
A/Reference number: S34268
A/Accession: S34268
A/Molecule type: mRNA
A/Residues: 1-307 <RA>
A/Cross-references: EMBL:X73138; NID:9312661; PIDN:CAA51653.1; PID:9312662
R/Agulla, H.; Link, T.A.; Klingenberg, M.
EMBO J. 4, 2369-2376, 1985
A/Title: The uncoupling protein from brown fat mitochondria is related to the mito
A/Reference number: A24363; MUID:86081749; PMID:3000775
A/Accession: A24363
A/Molecule type: protein
A/Residues: 2-128, 130-307 <AO>

A/Note: 128-Phe was also found
 R/Winkler, E.; Klingenberg, M.
 Eur. J. Biochem. 203, 295-304, 1992
 A/Title: Phococaffinity labeling of the nucleotide-binding site of the uncoupling protein
 A/Reference number: S20294; MUID:92111578; PMID:1730236
 A/Accession: S20294
 A/Molecule type: protein
 A/Residues: 257-307 <MIN>
 R/Bockerskorn, C.; Klingenberg, M.
 FEBS Lett. 226, 166-170, 1987
 A/Title: In the uncoupling protein from brown adipose tissue the C-terminus protrudes to
 A/Reference number: S02427; MUID:88083626; PMID:3691813
 A/Accession: S02427
 A/Molecule type: protein
 A/Residues: 300-304 <ECK>
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein
 F/10-103/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F/209-296/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 Query Match 58.1%; Score 915.5; DB 2; Length 307;
 Best Local Similarity 57.6%; Pred. No. 3.5e-71;
 Matches 179; Conservative 51; Mismatches 70; Indels 11; Gaps 4;
 Db 1 MWGFKATDVPPATVVKFLAGTACIADLTFPLDTAKVRLQIGESQGPVATASQYR 60
 1 MNPPTSEVHPFMGVIFSGVAAACIADLTFPLDTAKVRLQIGESQ----ISSTIRYK 56
 QY 61 GVGNTITLTVRTGEPSSLNGLVAGLQRMSPASVATIGLYDSVKPFTYKGS-NHSTGR 119
 Db 57 GVGITITLTAKEGLPLVSGLPAGIQRIQISFASLIGLYDVQGFESSGKTEPTLGNR 116
 QY 120 LLAGSTGALAAVAAPDTPVVKRPOAARAGGGR-RYOSTVNAKYTIAREGFRGLMKG 178
 Db 117 ISAGLMTGVAVFPGQTEVYKRLQASHHGKIKRYGTNARIATTESFETLWKG 176
 QY 179 TSPVNAENAVNCAELVYDILKDALIKANLMTDDIPCHFTSAFAGAGCTTYASPDVY 238
 Db 177 TTPMLRNVILNCELVETVYDLMKGAIVNNOIADVPCHILSAFVAGFCTTFLASPADV 236
 QY 239 KTRVNSALGOYSAGHCALTMLOKSGRAFYKGFPSFLRLGSNNVMMFVTEYQLKAL 298
 Db 237 KTRFINSPPGQYPSVPCAMTMTLKSGPTAFKGFVPSFLRLASNNVIMFVCEQLKEL 296
 QY 299 MAA-----CTS 304
 Db 297 SKSRQTVDCCT 307

RESULT 5
 G01858
 uncoupling protein 1, mitochondrial - human
 N/Alternate names: UCPI
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 20-Jun-2000
 C/Accession: G01858; S78473; S29141; A60793; A45763
 R/Bouilland, F.
 submitted to the EMBL Data Library, June 1995
 A/Reference number: G08642
 A/Accession: G01858
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-307 <BOU1>
 A/Cross-References: EMBL:U28480; NID:G1155218; PIDN:AA85271.1; PID:G1155219
 A/Accession: S78473
 A/Molecule type: DNA
 A/Residues: 1-20, 'P', 22-307 <BOU2>
 A/Cross-References: EMBL:X51952; NID:937606; PIDN:CAA6214.1; PID:G1177311
 R/Cassard, A.M.; Bouilland, F.; Mattei, M.G.; Hentz, E.; Raimbault, S.; Thomas, M.; Ricq
 J. Cell. Biochem. 43, 255-264, 1990
 A/Title: Human uncoupling protein gene: structure, comparison with rat gene, and assignm
 A/Reference number: A45763; MUID:90338166; PMID:2380264

A/Accession: S29141
 A/Molecule type: DNA
 A/Residues: 1-20, 'P', 22-108, 'SK', 111, 113-133, 'S', 135-197, 'T', 199-216, 'U', 218-307 <C
 A/Cross-References: EMBL:X51952; NID:937606; PIDN:CAA6214.1
 R/Bouilland, F.; Villarroja, F.; Hentz, E.; Raimbault, S.; Cassard, A.M.; Rigulier,
 Clin. Sci. 75, 21-27, 1988
 A/Title: Detection of brown adipose tissue uncoupling protein mRNA in adult patient
 A/Reference number: A60793; MUID:88311701; PMID:3165741
 A/Accession: A60793
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 113-133, 'S', 135-196 <BOV>
 A/Comment: This protein is responsible for the generation of heat by brown fat.
 C/Genetics:
 A/Genes: GDB:UCP1, UCP
 A/Cross-References: GDB:128179; OMIM:113730
 A/Map position: 4q31-4q31
 A/Intons: 42/3; 109/1; 176/1; 210/1; 270/2
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: adipose tissue; duplication; mitochondrion; transmembrane protein
 F/10-103/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F/209-296/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 Query Match 58.1%; Score 915; DB 2; Length 307;
 Best Local Similarity 59.3%; Pred. No. 3.8e-71;
 Matches 178; Conservative 48; Mismatches 66; Indels 6; Gaps 3;
 Db 1 MWGFKATDVPPATVVKFLAGTACIADLTFPLDTAKVRLQIGESQGPVATASQYR 60
 1 MGLTASDVHPTLQGLPSAGAACIADLTFPLDTAKVRLQVGECP---TSVIRYK 56
 QY 61 GVGNTITLTVRTGEPSSLNGLVAGLQRMSPASVATIGLYDSVKPFTYKGS-NHSTGR 119
 Db 57 GVGITITLTAKEGLPLVSGLPAGIQRIQISFASLIGLYDVQGFESSGKTEPTLGNR 116
 QY 120 LLAGSTGALAAVAAPDTPVVKRPOAARAGGGR-RYOSTVNAKYTIAREGFRGLMKG 178
 Db 117 ISAGLMTGVAVFPGQTEVYKRLQASHHGKIKRYGTNARIATTESFETLWKG 176
 QY 179 TSPVNAENAVNCAELVYDILKDALIKANLMTDDIPCHFTSAFAGAGCTTYASPDVY 238
 Db 177 TTPMLRNVILNCELVETVYDLMKGAIVNNOIADVPCHILSAFVAGFCTTFLASPADV 236
 QY 239 KTRVNSALGOYSAGHCALTMLOKSGRAFYKGFPSFLRLGSNNVMMFVTEYQLKAL 298
 Db 237 KTRFINSPPGQYPSVPCAMTMTLKSGPTAFKGFVPSFLRLASNNVIMFVCEQLKEL 296
 QY 299 MAA-----CTS 304
 Db 297 SKSRQTVDCCT 307

RESULT 6
 A31106
 mitochondrial uncoupling protein - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 21-Jul-2000
 C/Accession: A31106
 R/Kozak, L.P.; Britton, J.H.; Kozak, U.C.; Wells, J.M.
 J. Biol. Chem. 263, 12274-12277, 1988
 A/Title: The mitochondrial uncoupling protein gene. Correlation of exon structure
 A/Reference number: A31106; MUID:88315014; PMID:3410843
 A/Accession: A31106
 A/Molecule type: DNA; mRNA
 A/Residues: 1-306 <KOZ>
 A/Cross-References: GB:U63418; NID:G1519064; PIDN:AAB07367.1; PID:G1519065
 C/Genetics:
 A/Genes: Ucp
 A/Intons: 41/3; 108/1; 175/1; 209/1; 269/2
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein
 F/9-102/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F/109-201/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F/208-295/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 Query Match 57.8%; Score 911.5; DB 2; Length 306;

Best Local Similarity 58.0%; Pred. No. 7.6e-71;
Matches 177; Conservative 53; Mismatches 64; Indels 11; Gaps 4.

```

QY      7 TDVPNATYKFLDAGTAACIADIITFEDLTAAVRLQIQIGESQGVRAATASQYRWGWTI 66
  QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      6 SEVQPMGVKXIFSAGVSACTLADITTFPDTAKVRLQIQEGQ---ASSTRKXGVLTGI 61

QY      67 LTMWRTEGSPSLINGVLVAGLQRMSTASRILYLYSVNQFOTKQSE-HASIGSLLAGST 125
  QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62 TTIKTEGRLPKYISGLPAGIQRQISASIRLILYQSVETVSGSETPASIGNKISGLM 121

QY      126 TGAIAVAVAOPTDVVVVRFQQAARAQGRS-RYQSTVNAKYKTIAREEGFRGLMKQTSBNVA 184
  QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      122 TGGVAVFIQGPTEVVVVKVRMQAOGHLHGIRPKRYTGTYNVAVYALTTESLTIKMGTPENLM 181

QY      185 RNLIVNCAELWYTDLLKDALIKRANMTDDLPOHFIASAGAGCTVTVASPDVYKTEYNM 244
  QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182 RNVIINCTELVYTDLMKCALVNNKILADIVPCHLILSALVAGFCITLLASPDVYKTFIN 241

QY      245 SALGOYSSACHALITMLQREGPRAFYKGFMSFLRIGSNVVMFVYEQLRALMAA-- 301
  QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      242 SLRQOYPSVPSCAMSWYTKEGPAPFVKGVASFLRLIGSNVVMIFVCEQOLKKEIMKSRQT 301

QY      302 --CTS 304
  QY      : : :
Db      302 VDCIT 306

```

RESULT

uncoupling protein - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Jun-2000

R; Casteilla, L.; Bouillaud, F.; Forest, C.; Ricquier, D.

A1: Title: Nucleotide sequence of a cDNA encoding bovine brown fat uncoupling protein. Hom
A1: Reference number: S03603; MID:89183626; PMID:2928121

A;Molecule type: mRNA
A;Residues: 1-288 <CDS>

R;Ricquier, D.
submitted to the EMBL Data Library, January 1985

A;Accession: S05075
A;Molecule type: mRNA

C1; Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

F1;92-187/Domain: ADP,ATP carrier protein repeat homology (Fragment) <ACPi>
F1;92-184/Domain: ADP,ATP carrier protein repeat homology <ACP2>

Query Match	Score	DB 2	Length
57.6%;	907.5;	DB 2;	Length 288;

```

      Bseq LocalSimilarity 02:59, Etree: no, loc: 70,
Matches 175; Conservative 49; Mismatches 50; Indels 7; Gaps 4
QY   AGTACACADATVITPPDPTAKVRLOIGESGSPFAPASAOYRGWAGTILLTVRTGESRLY 79
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    4  AGVACACADATVITPDLTKVRLOIGE-----CLISARIRGVLTGITLLTKREGSVKLY 59
QY   80 NGVLAVGLQRQWFSEAFSAYRIGLYDSVKQFYTKGEHSAIGSSLBAGSTTGALAAVAAPTDV 139
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    60 SGLPAGLQRQSLASLRIGLYDTVGVEFFITGKE-ASLSKSIAGLMGTGAAPVLIQPTREV 118
QY   140 VKVFQQAQAPAGGR-RYGSTYNAYKTILAREGEFGMLKGTSPNVANNAIVNCAELVTVD 198
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    119 VKVRLAQSHLHGFKPRRYGTNAVRIIILTTEGLTGLMKGTSPMLTNVINLTETLVATD 178
QY   199 LIKALLKANLMTDDLPCHFTSAFGAGFCCTTYIASPVYVWVTRRWMSNALQYSAGHQL 258
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

```

Db 179 LKAEALVKNKLLADVDPCHEFVSAVVAAGCTTYLSSPVVDVYKTRFVSSPGQNTSVPCAM 238
Qy 259 TMLQEGEPRAFYKGFMPSLRLGSNNVMFTVTEYLKRLM 299
Db 239 MMLTRGPGSAFEEKGVPSPFLRLGSNN-IMFVCFEELKQELM 278

RESULT 8

uncoupling protein [imported] - Arabidopsis thaliana
N:Alternate names: protein F24B22.70
C:Species: Arabidopsis thaliana (mouse-ear cress)

C/Accession: T47570; T52023
R/Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salancubal, M.

A:Reference number: Z23016
A:Accession: T47570

A:Molecule type: DNA
A:Residues: 1-306 <BLO>

A: Experimental source: cultivar Columbia; BAC clone F24B22
R: Laloi, M.

A;Reference number: Z25905
A;Accession: T52023

A;Molecule type: mRNA
A;Residues: 1-306 <LAL>

A;Map position: 3

C/Superfamily: ADP,ATP carrier protein, ADP,ATP carrier protein repeat homology

Query Match	Score	DB 2	Length
Best Local Similarity	44.0%;	693.5;	306;
	50.0%;	Pred. No. 4.4e-52;	

	Matches	15	Conserved	45	Nonconserved	97	Insert	22	Deletion
QY	17	FLGAGVACTADITLPBLDTAKRRLIQGES--QGPVRAVSAQYNGVNGVITLIMVTRBGP	75						
DB	15	PACAFAPACAGEVCTITPLDTAKRRLQLOKSALAGV--TLPKYGLLGITGTTAREBGL	71						
QY	76	RSLLNGVLVAGLQRMSPASVRIQLDYDVQFYTKSEHNS--IGSRLLASITTGALAVA	133						
DB	72	RLTKGVAVPGLHQCFEGGLRIIMYEPVNLVY-GKDFVGDVPLSKTILAGITLGAIGIM	130						
QY	133	VAGCTDVAKRFAQALR--AGGGRKQSTVNAVYKTIAREEGRGKMGKSPVAVANAIVN	190						
DB	131	VANPTDLYKRLQAEGTLAAGAPRRKISGALNNYSTIVREGVRAIMTGLGPRVANAIIIN	190						
QY	191	CAELVYDILKDALIKANLMTDLPCHFSASAGAGCTTVIASPVDVYKTRPMNSALQY	250						
DB	191	AAELASVDQVETLLKPGFTDNVVTHLISGLQAGFAVCISPPVDVYKSRMGDS--GAY	24						
QY	251	SSAGHCALIMLOKEGPRAFYKGPMSFLRLGSMNVVMFVYIQOLR	296						
DB	250	KGITDCEFKTLKSDGPAFYKGFILNFGSLGSMNVIMFLLIQAK	295						

RESULT

uncoupling protein [imported] - *Arabidopsis thaliana*
152024
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence revision 20-Oct-2000 #text change 03-Nov-2000

C/Accession: 152024
R/Mia, I.G.; Benedetti, C.E.; Leite, A.; Turcinelli, S.R.; Vercosi, A.E.; Arruda, F.F.S. Lett. 429, 403-406, 1998

A:Accession: T52024
A:Title: ATP6MF: an *At*ADADopsis gene encoding a plant uncoupling
A:Reference number: Z22968; MUID:9662458; PMID:9662458

Query Match 30.7%; Score 483.5; DB 2; Length 313;
 Best Local Similarity 34.8%; Pred. No. 5.2e-34;
 Matches 106; Conservative 59; Mismatches 117; Indels 23; Gaps 3;

17 FLGAGTACIADLITFPDITAKVRLQIQESGCP-----VRATAS 56
 6 FVEGGIASVINGCSTHPLDLIKVRLQHGEPSTTTTLRPAALFPPSSPAFLFETTS 65

57 AQRNGVMTITLMTRESPRLNGVAGLQRMSPFSAVIGIYDVKQFYT-KGSEHNS 115
 66 VPKVGFISLGINIVKSEGAALFSGVSAATLRQTLYSTMGLEYELKKNWIDPESKJIN 125

116 IGSRLAGSTTGALAAVAOFTDVVKVRFQOAR--AGGRRYOSTVNAVKTIAREEGR 173
 126 LSRKTGAGLVAGIGCAVGNPADVAMRMQADGRLLPLAQRNVAAGVDALRSVKEGVKT 185

174 GIMKGTSPNVAARNALVNCALVITDILKDALIKRANLMTDLPCHFTSAFAGCCTIVAS 233
 186 SLMRGSALTINRAMITVAQLASYPQFEGILENGVNNDELGTHVVASFAAGFVASVSN 245

234 PVDVVKTRVYNSALGQYSAGCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVFYTYEQ 293
 246 PVDVVKTRVYNSALGQYSAGCALTMLOKEGPRAFYKGFMPSPFLRGSNNVVFYTYEQ 305

294 IKRAL 298
 306 VRKLL 310

RESULT 13
 DB613
 Hypothetical protein At2g2500 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C/Accession: D84613
 R/Lin: X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
 Eues, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: D84613
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1313 <STO>
 A/Cross-references: GB:AE002093; NID:94544443; PIDN:AAD22351.1; GSPDB:GN00139
 A/Map position: 2
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 30.2%; Score 475.5; DB 2; Length 313;
 Best Local Similarity 35.9%; Pred. No. 2.5e-33;
 Matches 108; Conservative 57; Mismatches 115; Indels 21; Gaps 4;

17 FLGAGTACIADLITFPDITAKVRLQIQES-----QGPVATASAOYRGV 63
 6 FAEGGIASIVAGSTHPLDLIKVRLQHGEPSTTTTLRPAALFQSTTVNAPPLRAGVI 65

64 GTLLMTVTRTEGPRSLNGVAGLQRMSPFSAVIGIYDVKQFYT-KGSEHNSIGSRLA 122
 66 GVGSRILIREGMAALFSGVSAATLRQTLYSTMGLEYELKKNWIDPESKJIN 125

123 GSTTGALAAVAOFTDVVKVRFQOAR--AGGRRYOSTVNAVKTIAREEGRGIMKTS 180
 126 GALAGALGAIVGNPADVAMRMQADGRLLPLAQRNVAAGVDALRSVKEGVKT 185

181 PNVARNALVNCALVITDILKDALIKRANLMTDLPCHFTSAFAGCCTIVASPDVKT 240
 186 LITNRAVLVTSQIASVSKETILKGLKQGLGTHVASFAAGFVASVSNPVDVKT 245

241 RYNN-----SALQYSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSNNVVFYTYEQ 295

DB 246 RYNNMKVAVGAPYKGAADCAKTKVAKGIMSLYKGFIPVYSRQAPFTVLAFTLEQVK 305
 QY 296 R 296
 DB 306 K 306

RESULT 14
 H86274
 FTA19.22 protein - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
 C/Accession: H86274
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar
 asen, N.F.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marz
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, U.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tai
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: H86274
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-305 <STO>
 A/Cross-references: GB:AE005172; NID:G5080790; PIDN:AAD39300.1; GSPDB:GN00141
 C/Genetics:
 A/Map position: 1
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 29.6%; Score 466; DB 2; Length 305;
 Best Local Similarity 34.6%; Pred. No. 1.6e-32;
 Matches 107; Conservative 58; Mismatches 126; Indels 18; Gaps 7;

5 KATVPPATVYKFLGACTACIADLITFPDITAKVRLQIQESGCPVATASAOYR-GVM 63
 5 RVTNEAPVGT-RILASLSMVAHSVTFPDLTKTMQLHGS-----SASAGARIGAF 57

64 GTLLMTVTRTEGPRSLNGVAGLQRMSPFSAVIGIYDVK-----QFYKGEHNSIGSR 119
 58 GVSEIARKEGVIGLVGLSPALIRHLYFPPIRIGENKGLIVSETNNSLPLATK 117

120 LLAGSTGALAAVAOFTDVVKVRFQOAR--AGGRRYOSTVNAVKTIAREEGRGLW 176
 118 ALVGGFSGVIAQVVASPADLVKRMQADGRLLVQGLKPRYSPIEAFKILQSEGVKIM 177

177 KGTSPNVAARNALVNCALVITDILKDALIKRANLMTDLPCHFTSAFAGCCTIVASPD 236
 178 KGVLENIORAFVLMVNGELACVDAKHVVIDIKKIAEDNIFVHTLASIMSGLASTSLSPAD 237

237 VKTRVYNSALGQ-YSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSNNVVFYTYEQ 295
 238 VKTRVYNSALGQ-YSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSNNVVFYTYEQ 297

296 PALMAACTS 304
 298 --LLAGISS 304

RESULT 15
 T25459
 Hypothetical protein B0432.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C/Accession: T25459
 R/Henkhaus, J.; Wohlmann, P.
 submitted to the EMBL Data Library, December 1996
 A/Description: The sequence of C. elegans cosmids B0432.
 A/Reference number: Z20038

A:Accession: T25459
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1323 <H2N>
 A:Cross-references: EMBL:U80836; PIDN:AA37890.1; GSPDB:GN00020; CESP:B0432.4
 A:Experimental source: strain Bristol N2; clone B0432
 C:Genetics:
 A:Gene: CESP:B0432.4
 A:Map position: 2
 A:Initrns: 20/2; 99/2; 149/1; 254/3; 306/2
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 Query Match 28.3%; Score 446.5; DB 2; Length 323;
 Best Local Similarity 33.2%; Pred. No. 8.3e-31;
 Matches 99; Conservative 54; Mismatches 132; Indels 13; Gaps 3;
 QY 15 VKFLGAGTACIADLTFFPLDTAKVRLQIGESQGPVRATASAOYRGVWGTLTWRTG 74
 DB 11 VKFAPGGTAGMGATLVVQPLDVKNKQLSG-----TTGKKEYRSSMHALTSIMKNG 63
 QY 75 PRSLVNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRIAGSTTGALAVVA 134
 DB 64 VFAYVNGLSAGLRQATYTTTRLTGYAFILERTKDKPLSFQMKAVLGMTAGIGISFVG 123
 QY 135 QPTDVVAVRFOAQR--AGGGRYQSTVNAKTIAREGFRGLWKGTSPNVARNAIVNCA 192
 DB 124 TPAETILIRMTGDRLEVEQRNRYTGVNALTRITKEBGLTLMRGCTPTVLRANVNA 183
 QY 193 ELVTVYDLIKDALKANIMTDLDPQHFTSAFGAGCTTVIASPVVVKTRYMNSAL---G 248
 DB 184 QLATYSQAKQALLASGVQDGI FCHFLASWISGLATTIASMPVDIAKRIQSMKVIDGKP 243
 QY 249 QYSSAGCALTMLQKGPRAFYKGFMPSPFLGSMNVVMFVYEQLKRALMAACTSEE 306
 DB 244 EYKNAFDVWGKVIKNBGI FALWKGFTPYWRLGPHTVLTFILIQWNAAYFOYVLKRD 301

Search completed: February 4, 2004, 09:19:56
 Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 09:15:43 ; Search time 41 Seconds
(without alignments)
1944.835 Million cell updates/sec

Title: US-09-884-814-1
Perfect score: 1576
Sequence: 1 MWGFKATDVPPATVTKFLGA.....TYEQIKRALMAACTSREAPP 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phase:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP Vertebrate:*
14: SP Unclassified:*
15: SP_rvinnus:*
16: SP_bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1519	96.4	309	11 Q9R246	Q9R246 mus musculus
2	1502	95.3	309	11 Q8CBUC	Q8CBUC mus musculus
3	1500	95.2	309	11 Q9ER17	Q9ER17 phodopus su
4	1320	83.8	273	6 Q9XSE1	Q9XSE1 bos taurus
5	1141.5	72.4	299	11 Q9ER16	Q9ER16 phodopus su
6	1114	70.7	307	13 Q9DX50	Q9DX50 meleagris g
7	1109	70.4	307	13 Q9DPT7	Q9DPT7 gallus gall
8	1106	70.2	307	13 Q8AYM4	Q8AYM4 gallus gall
9	1085.5	68.9	304	13 Q8BR90	Q8BR90 eupetomena
10	965	61.2	309	6 Q9GMZ1	Q9GMZ1 canis famli
11	901.5	57.2	307	11 Q8K404	Q8K404 dicostonyx
12	899.5	57.1	307	11 Q9ER18	Q9ER18 phodopus su
13	852.5	54.1	224	13 Q8QG96	Q8QG96 pagrus majo
14	745.5	47.3	154	6 Q9NID9	Q9NID9 macaca mula
15	695.5	44.1	300	10 Q9AVG1	Q9AVG1 oryza sativ
16	693.5	44.0	306	10 Q81845	Q81845 arabidopsis

17	693	44.0	310	10 Q8S4C4	Q8S4C4 zea mays (m
18	687	43.6	304	10 Q8JNZ1	Q8JNZ1 heliodicer
19	684.5	43.4	193	6 Q9NID8	Q9NID8 macaca mula
20	684.5	43.4	303	10 Q85623	Q85623 arabidopsis
21	674.5	42.8	306	10 Q9MBE7	Q9MBE7 symplocarpu
22	671.5	42.6	306	10 Q24391	Q24391 solanum tub
23	670.5	42.5	306	10 Q8S4S8	Q8S4S8 lycopersico
24	619.5	39.3	305	10 Q8ZMG1	Q8ZMG1 arabidopsis
25	616	39.1	293	10 Q9AVG2	Q9AVG2 oryza sativ
26	601.5	38.2	286	10 Q9FX05	Q9FX05 triticum ae
27	594	37.7	268	10 Q9MBE6	Q9MBE6 symplocarpu
28	593.5	37.7	286	10 Q9FX06	Q9FX06 triticum ae
29	543.5	34.5	241	10 Q8W1A4	Q8W1A4 glycine max
30	541.5	34.4	242	10 Q94T06	Q94T06 mangifera i
31	538	34.1	241	10 Q8W1A3	Q8W1A3 glycine max
32	522	33.1	291	6 Q8HX3	Q8HX3 macaca fasc
33	520.5	33.0	322	11 Q9JMH0	Q9JMH0 rattus norv
34	520.5	33.0	325	11 Q9EP88	Q9EP88 rattus norv
35	520	33.0	291	11 Q9CR58	Q9CR58 mus musculu
36	517.5	32.8	352	11 Q8CU24	Q8CU24 mus musculu
37	517.5	32.8	356	11 Q8CU23	Q8CU23 mus musculu
38	517.5	32.8	155	6 Q9NID0	Q9NID0 macaca mula
39	500.5	31.9	155	6 Q9TTL1	Q9TTL1 canis famli
40	495	31.8	141	6 Q9VX14	Q9VX14 drosophila
41	486	30.8	322	11 Q9EPH7	Q9EPH7 rattus norv
42	484.5	30.7	313	10 Q8LDF6	Q8LDF6 arabidopsis
43	483.5	30.7	313	10 Q9SBS2	Q9SBS2 arabidopsis
44	479.5	30.4	303	5 Q9TWM8	Q9TWM8 drosophila
45	476	30.2	322	11 Q9D6D0	Q9D6D0 mus musculu

ALIGNMENTS

RESULT 1

Q9R246 PRELIMINARY; PRT; 309 AA.
ID Q9R246
AC Q9R246;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Uncoupling protein 2.
GN UCP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAST/EL;
RX MEDLINE=99269912; PubMed=10337618;
RA York B., Truett A.A., Monteliro W.P., Barry S.U., Warden C.H.,
RA Naggert J.K., Maddatu T.P., West D.B.;
RT "Gene-environment interaction: a significant diet-dependent obesity
RT locus demonstrated in a congenic segment on mouse chromosome 7.";
RT Mamm. Genome 10:457-462(1999).
RL -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -1-
DR EMBL; AF111999; AAD17199.1; -;
DR MGD; MGI:105354; Ucp2.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 309 AA; 33315 MW; B09794EBA99810F0 CRC64;

Query Match 96.4%; Score 1519; DB 11; Length 309;
Best Local Similarity 96.4%; Pred. No. 6,8e-120;
Matches 298; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

1 MWGFKATDVPPATVTKFLGAGTACACADITPTLTATYRRLQIOESGSPFRTATSAQYR 60
|||||

Db 1 MGFKATDVPPATVTFKFLGAGTACIADITFPDITAKVRLQIQESQGLVRTASQYR 60
 QY 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDVSKQFYTKGSEHAGISRL 120
 Db 61 GVLGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDVSKQFYTKGSEHAGISRL 120
 QY 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 Db 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 QY 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 Db 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 QY 181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 Db 181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSEFLGSMNVVMFTYEQLRALMA 300
 Db 241 RYNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSEFLGSMNVVMFTYEQLRALMA 300
 QY 301 ACTSREAPF 309
 Db 301 ACTSREAPF 309

RESULT 2

Q8CBU0 PRELIMINARY; PRT; 309 AA.
 ID Q8CBU0
 AC Q8CBU0;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Uncoupling protein 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RL EMBL; AK035298; BAC29022.1;
 DR EMBU; AK035298; BAC29022.1;
 SQ SEQUENCE 309 AA; 33388 MW; 6E6454DAC14D99DE CRC64;

Query Match

Best Local Similarity 95.3%; Score 1502; DB 11; Length 309;
 Matches 296; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGFKATDVPPATVTFKFLGAGTACIADITFPDITAKVRLQIQESQGLVRTASQYR 60
 Db 1 MGFKATDVPPATVTFKFLGAGTACIADITFPDITAKVRLQIQESQGLVRTASQYR 60
 QY 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDVSKQFYTKGSEHAGISRL 120
 Db 61 GVLGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDVSKQFYTKGSEHAGISRL 120
 QY 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 Db 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 QY 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 Db 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 QY 181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 Db 181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSEFLGSMNVVMFTYEQLRALMA 300
 Db 241 RYNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSEFLGSMNVVMFTYEQLRALMA 300
 QY 301 ACTSREAPF 309
 Db 301 ACTSREAPF 309

Db 301 AYESREAPF 309

RESULT 3

Q9ER17 PRELIMINARY; PRT; 309 AA.
 ID Q9ER17
 AC Q9ER17;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Uncoupling protein 2.
 OS Podopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Podopus.
 OC NCBI_TaxId=10044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RC von Praun C.; Burkert M.; Gessner M.; Klingenspor M.;
 RA "Tissue-specific expression and cold-induced mRNA levels of uncoupling
 RT proteins in the Djungarian hamster."
 RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; AF271264; AAC33984.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 309 AA; 33359 MW; 9D9C4C1B169F2771 CRC64;

Query Match

Best Local Similarity 95.2%; Score 1500; DB 11; Length 309;
 Matches 294; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGFKATDVPPATVTFKFLGAGTACIADITFPDITAKVRLQIQESQGLVRTASQYR 60
 Db 1 MGFKATDVPPATVTFKFLGAGTACIADITFPDITAKVRLQIQESQGLVRTASQYR 60
 QY 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDVSKQFYTKGSEHAGISRL 120
 Db 61 GVLGTLITWRTGPRSLYNGLVAGLQRMSPASVRIGLYDVSKQFYTKGSEHAGISRL 120
 QY 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 Db 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 QY 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 Db 121 LAGSTGALAVAAOPTDVVKVRFQOAPRAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
 QY 181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 Db 181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSEFLGSMNVVMFTYEQLRALMA 300
 Db 241 RYNSALGOYSSAGHCALITMLQKSGPRAFYKGFMPSEFLGSMNVVMFTYEQLRALMA 300
 QY 301 ACTSREAPF 309
 Db 301 ACTSREAPF 309
 QY 301 AYESREAPF 309
 Db 301 AYESREAPF 309

RESULT 4

Q9XSE1 PRELIMINARY; PRT; 273 AA.
 ID Q9XSE1
 AC Q9XSE1;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Uncoupling protein 2 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.
 RN NCBI_TaxID=9913;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Stone R.T., Rexroad C.E., Smith T.P.L.;
 RT "Bovine UCP2 and UCP3 map to BTAL5";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF212028; AAD29572.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carrier_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER.
 DR NON TER 1
 FT SEQUENCE 273 AA; 29638 MW; 40DAF6CB47AAB48 CRC64;
 Query Match 83.8%; Score 1320; DB 6; Length 273;
 Best Local Similarity 94.9%; Pred. No. 3,4e-103;
 Matches 259; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 37 AKVRLQIGESQGPATASQYRGVVMGTLITWRTGEPRLSYNGLVAGLQROMSFAVR 96
 DB 1 AKVRLQIGERQGMHQAASQYRGVLTITWRTGEPRLSYNGLVAGLQROMSFAVR 60
 QY 97 IGLYDVAKQFTTKGSEHASISGRLAAGTTGALAVVAOPTDVYKVRFOAQRAGGRRY 156
 DB 61 IGLYDVAKQFTTKGSEHASISGRLAAGTTGALAVVAOPTDVYKVRFOAQRAGGRRY 120
 QY 157 QSTVNAVYKTIARESGPRGIMKGTSPNVAARNVNCALVLYDILKDALIKANLMTDDLP 216
 DB 121 QSTVNAVYKTIARESGPRGIMKGTSPNVAARNVNCALVLYDILKDALIKANLMTDDLP 180
 QY 217 HFTSAFGAGFCTTYIASPVYVYKRYNSALGQYSSAGHCALTMLOKSGPRAFYKGFMP 276
 DB 161 HFTSAFGAGFCTTYIASPVYVYKRYNSALGQYSSAGHCALTMLOKSGPRAFYKGFMP 240
 QY 277 FLRLGSNNVVMFVTEQKRALNMACTSRAPF 309
 DB 241 FLRLGSNNVVMFVTEQKRALNMACTSRAPF 273
 RESULT 5
 QSER16 PRELIMINARY; FRT; 299 AA.
 ID QSER16
 AC QSER16;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 3 (Fragment).
 OS Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Phodopus.
 OC NCBI_TaxID=10044;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Tissue-Brown adipose tissue;
 RA von Praun C., Burkert M., Gesener M., Klingenspor M.;
 RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling
 proteins in the Djungarian hamster";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF21265; AAG33985.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carrier_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER. 3.
 KW Membrane; Transmembrane; Transport.
 FT NON TER 299
 FT SEQUENCE 299 AA; 32784 MW; AB5C947B4DDC49A0 CRC64;

Query Match 72.4%; Score 1141.5; DB 11; Length 299;
 Best Local Similarity 73.4%; Pred. No. 4,2e-88;
 Matches 221; Conservative 33; Mismatches 40; Indels 7; Gaps 3;
 QY 1 NVGFATDVPPATATKFLGAGTACIADLTTPDTRKVKLOIQSGSPVATASQYR 60
 DB 1 NVGLQSPVPPATATKFLGAGTACIADLTTPDTRKVKLOIQSGSPVATASQYR 56
 QY 61 GVMGTLITWRTGEPRLSYNGLVAGLQROMSFAVRIGLYDVAKQFTT-KXSEHASISGR 119
 DB 57 GLVGLITWRTGEPRLSYNGLVAGLQROMSFAVRIGLYDVAKQFTT-KXSEHASISGR 116
 QY 120 LLAGSTGALAVVAOPTDVYKVRFOAQR--AGGGRYQSTVNAVYKTIARESGPRGLMK 177
 DB 117 LLAGCTGAMAVTCAQPTDVYKVRFOAMILGTERKRYGTDAYRTTARESGRGLMK 176
 QY 178 GTSPPVARNALVNCALVLYDILKDALIKANLMTDDLPCHFTSAFGAGFCTTYIASPV 237
 DB 177 GTWPNITRNALVNCALVLYDILKDALIKANLMTDDLPCHFTSAFGAGFCTTYIASPV 236
 QY 238 VTRRYNSALGQYSSAGHCALTMLOKSGPRAFYKGFMPFLRGSNNVVMFVTEQKRA 297
 DB 237 VTRRYNSALGQYSSAGHCALTMLOKSGPRAFYKGFMPFLRGSNNVVMFVTEQKRA 296
 QY 298 L 298
 DB 297 L 297

RESULT 6

Q90X50 PRELIMINARY; FRT; 307 AA.
 ID Q90X50
 AC Q90X50;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein UCP.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OC NCBI_TaxID=9103;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Tissue-Skeletal muscle;
 RA Ewok-Clover C.M., Pech S.M., Richards M.P.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF436811; AAL28138.1;
 DR InterPro; IPR000794; Ketocyl-synt.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001950; TIF_SUI1.
 DR Pfam; PF00153; mito_carrier_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE. 1.
 DR PROSITE; PS00215; MITOCH_CARRIER. 3.
 DR PROSITE; PS01118; SUI1. 1.
 SQ SEQUENCE 307 AA; 33148 MW; 256566D6B82ECCC CRC64;
 Query Match 70.7%; Score 1114; DB 13; Length 307;
 Best Local Similarity 71.0%; Pred. No. 9,1e-86;
 Matches 220; Conservative 34; Mismatches 50; Indels 6; Gaps 4;
 QY 1 NVGFATDVPPATATKFLGAGTACIADLTTPDTRKVKLOIQSGSPVATASQYR 60
 DB 1 NVGLQSPVPPATATKFLGAGTACIADLTTPDTRKVKLOIQSGSPVATASQYR 59
 QY 61 GVMGTLITWRTGEPRLSYNGLVAGLQROMSFAVRIGLYDVAKQFTT-KXSEHASISGR 119
 DB 60 GVLGTLITWRTGEPRLSYNGLVAGLQROMSFAVRIGLYDVAKQFTT-KXSEHASISGR 119

QY 120 LLAGSTTGALAAVAOPTDVVKRFOA-QAPAGGGRYOSTNAKYTIAEEGFRGLMG 178
 DB 120 LLAGCTGAAVAATCAOPTDVVKRFOALGALPESNRKRYSGVAVARIATIAEEGVRGLMG 179
 QY 179 TSPNARNAIVNCAELVYDILIKALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDV 238
 DB 180 TLPNTARNIINGELVYDILIKOTLLRAQIMTDNVCHPFAAFGAGFCATVVASPVDV 239
 QY 239 KTRYNMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRGSNNVVFVTEYOLKRAL 298
 DB 240 KTRYNMNSPQYRNVPSCILALIMODGISGLYKGFVPSFLRGSNNVVFISYEQLOQRYV 299
 QY 299 MAACTSREAP 308
 DB 300 MAA--RSAP 306

RESULT 7

Q9DDT7 PRELIMINARY; PRT: 307 AA.

AC Q9DDT7; PRELIMINARY; PRT: 307 AA.
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Mitochondrial uncoupling protein.
 GN UCP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=21092869; PubMed=11171038;
 RA Raimbault S., Dridi S., Denjean F., Lachner J., Couplan E.,
 RA Bouillaud E., Bordes A., Duchamp C., Taouis M., Ricquier D.;
 RT "An uncoupling protein homolog putatively involved in facultative
 RT muscle thermogenesis in birds";
 RL Biochem. J. 353:441-444 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Zhao J., Wang Q., Meng H., Gu Z., Li H.;
 RT "Cloning and Sequencing of Uncoupling Protein Gene in Chicken";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF287144; AAC48942.1; -;
 DR EMBL: AF433170; ALJ5325.2; -;
 DR InterPro: IPR000794; Ketcacyl-synt.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002087; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001950; TIF_SUI.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR PROSITE: PS01118; SUI1_1; 1.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 307 AA; 33130 MW; 33AC1CD66FC1A9CD CRC64;

Query Match

Best local similarity 70.4%; Score 1109; DB 13; Length 307;
 Matches 219; Conservative 35; Mismatches 50; Indels 6; Gaps 4;

QY 1 MVEGKATDVPTATVKFLGAGTAACIADLITPFLDTAKVRLQIGESQGPVATASQYR 60
 DB 1 MVEGKPEVPTATVKFSSAGTACIADLCTPFLDTAKVRLQIGEVRLP-RSTVTEYR 59
 QY 61 GVGSTILTVRTGPRSLVNGLVAGLORQMSFASVRIGLYDSVKQFTT-KGSEHASIGSR 119

DB 60 GVLGTLSTVWRTGPRSLVNGLVAGLORQMSFASVRIGLYDSVKQFTT-KGSEHASIGSR 119
 QY 120 LLAGSTTGALAAVAOPTDVVKRFOA-QAPAGGGRYOSTNAKYTIAEEGFRGLMG 178
 DB 120 LLAGCTGAAVAATCAOPTDVVKRFOALGALPESNRKRYSGVAVARIATIAEEGVRGLMG 179
 QY 179 TSPNARNAIVNCAELVYDILIKALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDV 238
 DB 180 TLPNTARNIINGELVYDILIKOTLLRAQIMTDNVCHPFAAFGAGFCATVVASPVDV 239
 QY 239 KTRYNMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRGSNNVVFVTEYOLKRAL 298
 DB 240 KTRYNMNSPQYRNVPSCILALIMODGISGLYKGFVPSFLRGSNNVVFISYEQLOQRYV 299
 QY 299 MAACTSREAP 308
 DB 300 MAA--RSAP 306

RESULT 8

Q8AYM4 PRELIMINARY; PRT: 307 AA.

AC Q8AYM4;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Uncoupling protein.
 GN AVUCP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
 RT and ANT mRNA in chicken skeletal muscle";
 RL FEBS Lett. 0:0-0(2002).
 DR EMBL: AB089865; BAB15532.1; -;
 RP SEQUENCE 307 AA; 33116 MW; 33AC1CD66FC1A888 CRC64;

Query Match

Best local similarity 70.2%; Score 1106; DB 13; Length 307;
 Matches 218; Conservative 36; Mismatches 50; Indels 6; Gaps 4;

QY 1 MVEGKATDVPTATVKFLGAGTAACIADLITPFLDTAKVRLQIGESQGPVATASQYR 60
 DB 1 MVEGKPEVPTATVKFSSAGTACIADLCTPFLDTAKVRLQIGEVRLP-RSTVTEYR 59
 QY 61 GVGSTILTVRTGPRSLVNGLVAGLORQMSFASVRIGLYDSVKQFTT-KGSEHASIGSR 119
 DB 60 GVLGTLSTVWRTGPRSLVNGLVAGLORQMSFASVRIGLYDSVKQFTT-KGSEHASIGSR 119
 QY 120 LLAGSTTGALAAVAOPTDVVKRFOA-QAPAGGGRYOSTNAKYTIAEEGFRGLMG 178
 DB 120 LLAGCTGAAVAATCAOPTDVVKRFOALGALPESNRKRYSGVAVARIATIAEEGVRGLMG 179
 QY 179 TSPNARNAIVNCAELVYDILIKALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDV 238
 DB 180 TLPNTARNIINGELVYDILIKOTLLRAQIMTDNVCHPFAAFGAGFCATVVASPVDV 239
 QY 239 KTRYNMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRGSNNVVFVTEYOLKRAL 298
 DB 240 KTRYNMNSPQYRNVPSCILALIMODGISGLYKGFVPSFLRGSNNVVFISYEQLOQRYV 299
 QY 299 MAACTSREAP 308
 DB 300 MAA--RSAP 306

RESULT 9

Q98T90

ID Q98790 PRELIMINARY; PRT; 304 AA.
 AC Q98790;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitochondrial uncoupling protein UCP.
 OS Eupetomena macroura (swallow-tailed hummingbird).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Aves; Neognathae; Trochiliformes; Trochilidae;
 OC Eupetomena.
 NCBI_TaxID=153633;
 OX NCBI_TaxID=153633;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vianna C.R., Hagen T., Zhang C.-Y., Bachman E., Boss O., Gereben B.,
 RA Miesco A.S., Lowell J.B., Bickel J.E.P.W., Bianco A.C.;
 RT "Cloning and functional characterization of an uncoupling protein
 homolog in hummingbirds";
 RL Physiol. Genomics (Online) 0:0-0(2001).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF555729; AAK16829.1; -;
 DR InterPro; IPR000794; Kctocyl-synt.
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001950; TIF_SUIT.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS01118; SUIL_1; 1.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 304 AA; 32833 MW; 3016453B21486795 CRC64;

Query Match 68.9%; Score 1085.5; DB 13; Length 304;
 Best Local Similarity 69.3%; Pred. No. 2,3e-83;
 Matches 210; Conservative 36; Mismatches 54; Indels 3; Gaps 3;

QY 1 MVGKATDVPPATATKFLGAGTAACIADLTTPFDATKVRLOIGESGQPVATASAOY 60
 DB 1 MVALKSGEMPTAIKRFSGAGTAACIADLTTPFDATKVRLOIGESVRLP-RVSGAVEH 59
 QY 61 GVMGTILMTVRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSYKQYTT-KSEHASIGR 119
 DB 60 GVLGTILMTVRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSYKQYTT-KSEHASIGR 119
 QY 120 LLAGSTGALAVAAQPTDVVKVRFQAGRRYOSTVNAKYTIAREGFRGLMK 178
 DB 120 LLAGCTGAVAAQPTDVVKVRFQAGRRYOSTVNAKYTIAREGFRGLMK 178
 QY 179 TSPVARNAINCAELVYDILKDALIKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 238
 DB 180 TLPATARNAINCAELVYDILKDALIKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 238
 QY 239 KTRVYNSALGOYSAGHCALMTLOKEGPRAFYKGFMSFRLGSMNVNMFVYEQLRAL 298
 DB 240 KTRVYNSALGOYSAGHCALMTLOKEGPRAFYKGFMSFRLGSMNVNMFVYEQLRAL 298
 QY 299 MAA 301
 DB 300 VLA 302

RESULT 10
 Q9GMZ1 PRELIMINARY; PRT; 309 AA.
 ID Q9GMZ1;
 AC Q9GMZ1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Uncoupling protein 1 UCP1.
 GN UCP1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishida K.;
 RT "Cloning of canine UCPs";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB046106; BAB11684.1; -;
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 309 AA; 33279 MW; C4D3352A3B08F16E CRC64;

Query Match 61.2%; Score 965; DB 6; Length 309;
 Best Local Similarity 62.9%; Pred. No. 3,3e-73;
 Matches 190; Conservative 44; Mismatches 62; Indels 6; Gaps 4;

QY 1 MGVKATDVPPATATKFLGAGTAACIADLTTPFDATKVRLOIGESGQPVATASAOY 59
 DB 1 MVRAPSDAPPTLSVRIAAAGAACIADLTTPFDATKVRLOIGESGQPVATASAOY 57
 QY 60 RGVMTILMTVRTEGPRSLYNGLVAGLQROMSPASVRIGLYDSYKQYTT-KSEHASIGR 118
 DB 58 RGVLTVALTARTEGPRSLYNGLVAGLQROMSPASVRIGLYDSYKQYTT-KSEHASIGR 117
 QY 119 LLAGSTGALAVAAQPTDVVKVRFQAGRRYOSTVNAKYTIAREGFRGLMK 177
 DB 118 RISAGVMTGAAVFIQOPTEVVKVRLQASHGKRPYTYTNAVRIATTEGLTGLMK 177
 QY 178 TSPVARNAINCAELVYDILKDALIKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 237
 DB 178 GTTPNLMRVITINCELTLYDILKDALIKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 237
 QY 238 VKTRVYNSALGOYSAGHCALMTLOKEGPRAFYKGFMSFRLGSMNVNMFVYEQLRAL 297
 DB 238 VKTRVYNSALGOYSAGHCALMTLOKEGPRAFYKGFMSFRLGSMNVNMFVYEQLRAL 297
 QY 298 LM 299
 DB 298 LM 299

RESULT 11
 Q8K404 PRELIMINARY; PRT; 307 AA.
 ID Q8K404;
 AC Q8K404;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Uncoupling protein 1.
 OS Dicrostonyx groenlandicus (northern collared lemming).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
 OC Dicrostonyx.
 NCBI_TaxID=85953;
 OX NCBI_TaxID=85953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22069795; PubMed=12075603;
 RA Powell C.S., Blaylock M.L., Wang R., Hunter H.L., Johanning G.L.,
 RA Nagy T.R.;
 RT "Effects of energy expenditure and Ucp1 on photoperiod-induced weight
 gain in collared lemmings";
 RL Obed. Res. 10:541-550(2002).
 DR EMBL; AF515781; AAM49148.1; -;
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW SEQUENCE 307 AA; 33530 MW; 78D492FD26D4897A CRC64;

Query Match 57.2%; Score 901.5; DB 11; Length 307;
 Best Local Similarity 56.9%; Pred. No. 7.4e-68;
 Matches 177; Conservative 52; Mismatches 71; Indels 11; Gaps 4;

QY 1 MGVGKATDVPPATVVFELGAGTACIADITPPLDTAKVRLQIQSGSPVATASQYR 60
 DB 1 MSLITSEVPTMVKVTFSGISACIADITPPLDTAKVRLQIQSGSQ----TSSTIRX 56
 QY 61 GVMGTTITMVRTGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQYTTGSE-HASIGSR 119
 DB 57 GVLGTTITLAKTEGMPKLYSGLPAGIQRIQISFASLIGLDTVQVEYFSSGKETPPLGKR 116
 QY 120 LLAGSTGALAAVAAPGTDVVKVRFQAGARAGGR-RYQSTVAAYKTIAREGFRGLMKG 178
 DB 117 ISAGLMTGVAVFIGQPLEVVKVRLQASHLHGKRYTQTNAYRIIATTSFSTLMKG 176
 QY 179 TSPVARNVAIVNCAELVYTDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIASPDVY 238
 DB 177 TTPNLMRVVIRNRELVYDLMKALVNNQIADVDYCHILSLVAGFCTTFLASPADVY 236
 QY 239 KTRVNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVMEVTEYQLKRAL 298
 DB 237 KTRFINSLPQYPSVSCAMTMTKEGPTAFKGFVPSFLRLASNNVIMFVCFQLKEL 296
 QY 299 MAA-----CTS 304
 DB 297 MMSRQTMDCCT 307

RESULT 12
 QSER18 PRELIMINARY; PRT; 307 AA.
 ID QSER18
 AC 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 1.
 OS Phodopus sungorus (Striped hairy-footed hamster) (Dungarian hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Phodopus.
 NC NCBI_TaxID=10044;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brown adipose tissue.
 RA von Praun C., Burkert M., Gessner M., Klingenspor M.:
 RA "Tissue-specific expression and cold-induced mRNA levels of uncoupling
 RT proteins in the Djungarian hamster."
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONRIAL CARRIER FAMILY.
 CC EMBL: AF271263; AAC33983.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 307 AA; 33364 MW; 7D9ED05FAB39709B CRC64;

Query Match 57.1%; Score 899.5; DB 11; Length 307;
 Best Local Similarity 56.6%; Pred. No. 1.1e-67;
 Matches 176; Conservative 51; Mismatches 73; Indels 11; Gaps 4;

QY 1 MGVGKATDVPPATVVFELGAGTACIADITPPLDTAKVRLQIQSGSPVATASQYR 60
 DB 1 MSLITSEVPTMVKVTFSGISACIADITPPLDTAKVRLQIQSGSQ----TSSTIRX 56
 QY 61 GVMGTTITMVRTGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQYTTGSE-HASIGSR 119
 DB 57 GVLGTTITLAKTEGMPKLYSGLPAGIQRIQISFASLIGLDTVQVEYFSSGKETPPLVNR 116
 QY 120 LLAGSTGALAAVAAPGTDVVKVRFQAGARAGGR-RYQSTVAAYKTIAREGFRGLMKG 178

DB 117 ISAGLMTGVAVFIGQPLEVVKVRLQASHLHGKRYTQTNAYRIIATTSFSTLMKG 176
 QY 179 TSPVARNVAIVNCAELVYTDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIASPDVY 238
 DB 177 TTPNLMRVVIRNRELVYDLMKALVNNQIADVDYCHILSLVAGFCTTFLASPADVY 236
 QY 239 KTRVNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVMEVTEYQLKRAL 298
 DB 237 KTRFINSLPQYPSVSCAMTMTKEGPTAFKGFVPSFLRLASNNVIMFVCFQLKEL 296
 QY 299 MAA-----CTS 304
 DB 297 MMSRQTMDCCT 307

RESULT 13
 Q08G96 PRELIMINARY; PRT; 224 AA.
 ID Q08G96
 AC Q08G96;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 2 (Fragment).
 OS Pagrus major (Red sea bream) (Chrysophrys major).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Pagrus.
 NC NCBI_TaxID=143350;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RA Liang X., Ogata H.Y., Oku H.:
 RA "Pagrus major mRNA for uncoupling protein 2."
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF487341; AAL92117.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 224 AA; 24686 MW; B8405F9D5A5B5D7 CRC64;

Query Match 54.1%; Score 852.5; DB 13; Length 224;
 Best Local Similarity 73.2%; Pred. No. 6.5e-64;
 Matches 164; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

QY 59 YRGVAGTILMVRTGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQYTTGSEHASIGS 118
 DB 1 YRGVAGTILMVRTGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQYTTGSKDNVLI 60
 QY 119 RLLAGSTGALAAVAAPGTDVVKVRFQAGARAGG-GRYQSTVAAYKTIAREGFRGLMK 177
 DB 61 RLLAGCTGAAVAFAPGTDVVKVRFQAGNNLGVARRYGTQAKYHIFQENGRGLMK 120
 QY 178 GTSNVARNVAIVNCAELVYTDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIASPDVY 237
 DB 121 GLPMTITNALVNTCELVYDLIKDALIKNLLSDNLPCHVAFGFGVTVIASPDVY 180
 QY 238 VTRVNSALGOYSAGHCALTMLOKEGPRAFYKGFMPSEFLRGL 281
 DB 181 VTRVNSPPOYKSALNCAMTMTKEGPTAFKGFVPSFLRLG 224

RESULT 14
 Q09ND9 PRELIMINARY; PRT; 154 AA.
 ID Q09ND9
 AC Q09ND9;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 2 (Fragment).

GN UCP2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Thompson G.M., Kelly L.J., Candelore M.R.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF202130; AAF34906.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr_2
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 KM Membrane; Transmembrane; Transport.
 FT NON_TER 1
 FT 154 154
 SQ SEQUENCE 154 AA; 16218 MW; BA0BEFC240C545EB CRC64;
 Query Match 47.3%; Score 745.5; DB 6; Length 154;
 Best Local Similarity 98.1%; Pred. No. 4e-55;
 Matches 152; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 4 FKATDVEPTATVFLGAGTACIADLITFPLDTAKVRLQIGESOGPVATASAGYRGVM 63
 DB 1 FKATDVEPTATVFLGAGTACIADLITFPLDTAKVRLQIGESOGPVATAGAYRGVL 60
 QY 64 GTLTWRTGEPRLNGVLVAGLQROMSTASVRLGLYDSVKQFTYKSEHASIGSRLLAG 123
 DB 61 GTLTWRTGEPRLNGVLVAGLQROMSPASVRLGLYDSVKQFTYKSEHASIGSRLLAG 120
 QY 124 STTGALAAVAVAOPTDVKKVFOQAARAGGRRYOS 158
 DB 121 STTGALAAVAVAOPTDVKKVFOQAARAGGRRYOS 154
 RESULT 15
 Q9AVG1 PRELIMINARY; PRT; 300 AA.
 ID Q9AVG1
 AC Q9AVG1
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Uncoupling protein.
 GN OSUCP2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Watanabe A., Hirai A.;
 RT "Two uncoupling protein genes are present in rice (*Oryza sativa*
 L.), but processing of their pre-mRNAs is defective."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB049998; BAB40658.1; -
 DR Gramene: Q9AVG1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr_3.
 DR PRINTS: PRO0926; MITOCARRIER.
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 31909 MW; A1ACBABS5457C592 CRC64;

Query Match 44.1%; Score 695.5; DB 10; Length 300;
 Best Local Similarity 48.4%; Pred. No. 1.ee-50;
 Matches 138; Conservative 49; Mismatches 87; Indels 11; Gaps 5;
 QY 16 KFLGAGTACIADLITFPLDTAKVRLQIGESOGPVATASAGYRGVMTLMTVTEGG 75
 DB 15 RFTASAIACFAEVCCTIPLDTAKVRLQLOKN---VAADAPKIRGLGTAIITABEGA 70
 QY 76 RSLYGLVAGLQROMSPASVRLGLYDSVKQFTYKSEHAS---IGSRLLAGSTTGALAVA 132
 DB 71 AALWKGIVPGLHRQCIYGLRLIGLYEYKSPYV-GKHVGDVPLTKKIAAGFTGAIAS 129
 QY 133 VAQPTDVKKRFOQAR-AGGGRYQSTVNAKYTLIABEGRGLMKGTSPNVAKNALVNC 191
 DB 130 IANPDLVKVRLQAGKLAIPARAYAGMDVAKIVRQBPALMTGIGNVARNALINA 189
 QY 192 AELVRYDLIKDALIKANLMTDDLPCHFSAFAGCTTVIASPVYVKTREYNMSALGOYS 251
 DB 190 AELASYDYVKQITLKPGRKDVVYTHLSGLGAGFPAVCVSPVDVYKSHMGDS--AYT 247
 QY 252 SAGHCALTMLQEGEFAFYKGFMPSPFLRISGNVVMFVYTBOLKR 296
 DB 248 STIDCFVKTLKNDGLAFYKGFLLPNFARLGSWNVIMFLTEQYOK 292
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